```
updates/sec
                                                                                                                                                                                                                                                                                                                                                                            /AA2001.DAT:*
/AA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                 to have
                                                                                   ....LIGGCLPWATRSHLGRRKCS 97
                                        Seconds
                                       Search time 54.0796 Sometry (without alignments) 239.005 Million cell
                                                                                                                                                                                                                                                                                                                                                                           /SIDS2/gcgdata/geneseq/geneseqp-embl/AA/SIDS2/gcgdata/geneseq/geneseqp-embl/AA
                                                                                                                                          908470
     Compugen Ltd
                                                                                                                                           Total number of hits satisfying chosen parameters
                                                                                                                            908470 seqs, 133250620 residues
                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                        EVEVSRDHASLGDSETLSQT.....
GenCore version
Copyright (c) 1993 - 2003
                             sw model
                                             9, 2003, 15:05:28;
                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                using
                                                                          US-09-854-133-586
                               OM protein - protein search,
                                                                                                                                                                                                                         July
                                                                                                            Scoring table:
                                                                                        score:
                                                                                                                                    Searched:
                                                                                                                                                                                                                      Database
                                                                                               Sednence:
                                                                                        Perfect
                                                    Run on:
```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Human polypeptide Human polypeptide	Human polypeptide	Human musculoskele uuman nervous syst	Mouse 5HT receptor Mouse G-protein co	Homo sapiens gluco
	ID		AAO04640 AAO09875			AAE03/40 AAE20598
		22	22	22	22.	22 23
	Length DB	16 121	46	163 66	63 423	423
ф	Query		13.4			12.8 12.8
	Score	866	71.5		60 60 60 60 60 60 60 60 60 60 60 60 60 6	
	Result No.	; ; ; ;	4 M 4	4 ru ,	0 r a	10

Active form of hum Human mutant G pro Human serotonin re Human protein sequu human protein sequu human secreted pro Human serotonin va Human serotonin va Human polypeptide Human polypeptide Human polypeptide human polypeptide plasmodium falcipa Novel human diagno common bean COK-4 Active form of hum Human serotonin re Invertebrate octop prosophila melanog Drosophila melanog prosophila melanog prosophila melanog prosophila melanog prosophila melanog human immune/haema Murine protein iso Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia	
458 20 AAY28851 458 21 AAY90676 458 22 AAB93643 105 22 AAB93643 105 22 AAB64601 458 17 AAR94577 458 19 AAW77108 458 21 AAY90641 64 22 AAO12091 116 22 AAO12091 116 22 AAO12091 116 22 AAY36632 64 22 AAY366719 83 22 ABG11242 100 22 AAG11242 369 23 AAM51135 478 22 AAB5135 637 20 AAY28853 478 22 AAB65096 642 20 AAY3680 642 20 AAY36896 1030 22 AAB60070 514 20 AAY65896 1030 22 AAB60070 177 21 AAG47017 184 21 AAG47015 189 22 AAU27511 213 21 AAG47015	
68 12.8 68 12.8 67 5 12.8 67 12.6 67 12.6 67 12.6 67 12.6 66.5 12.5 66.5 12.5 66.5 12.4 66 12.4	
11111111111111111111111111111111111111	

ALIGNMENTS

```
Benson DR, Indirias CY;
1, Mannion J, Kalos MD;
                                                                                                               Human; lung tumour protein; immunostimulant; cytostatic; gene therapy;
antisense-therapy; vaccine; immune response; lung cancer;
T cell epitope.
                                                                                         epitope related to lung tumour-specific protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Σ
                                                                                                                                                                                                                                                                                                                                                                                                                               Mohamath R, Secrist H, SP, Algate PA, Elliot
             AAE13851 standard; peptide; 16 AA
                                                                                                                                                                                                                                                                                                  29-MAR-2000; 2000US-0538037.
05-JUN-2000; 2000US-0588937.
18-AUG-2000; 2000US-0640878.
22-SEP-2000; 2000US-234517P.
01-NOV-2000; 2000US-0704512.
14-DEC-2000; 2000US-0738973.
                                                                                                                                                                                                                                                                           28-MAR-2001; 2001WO-US09991
                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Lodes MJ, Moha
RA, Fling SP,
                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
                                                                                                                                                                                                                        WO200172295-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Reed SG, Lode
Henderson RA,
                                                                                                                                                                                             Homo sapiens.
                                                                                                         Human T cell
                                                                                                                                                                                                                                                     04-OCT-2001.
                                                                               26-FEB-2002
                                                  AAE13851;
          AAE13851
RESULT
                                                                                                                                                                                                                                                                                                                               PR
PR
PR
                                                                                                                                                                                                                                                          PD
                                                                                                                                                                                                                                                                                                                   PR
                                                                                                                                                                                                                              PN
XX
                                                                                                               DE
```

. ;

```
peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human;
                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                    AAO04640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                      RESULT
                               8********
                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                 DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Κ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΡF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DR
XX
                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                     ting cancer. The
therapy and for
present sequence
                                                                                                                                                             inhibiting
a composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytokine; cell proliferation; cell differentiation; gene therapy;
e; peptide therapy; stem cell growth factor; haematopoiesis;
growth factor; immunomodulatory; cancer; leukaemia;
s system disorders; arthritis; inflammation.
                                                                                                                                        Proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to human polynucleotides (AAI79941-AAI93841) and encoded proteins (AAO00010-AAO13910) that exhibit activity elating to kine, cell proliferation or cell differentiation or which may induce fuction of other cytokines in other cell populations. The finucleotides and polypeptides are useful in gene therapy, vaccines or
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                              and
                                                              the
                                                                                                                           proteins
                                                                                                                                                                                                                             protein.
                                                                                                                                                     and
                                                                                                                                                                                                                                                                                                      ;
0
                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                solated nucleic acids and polypeptides, useful for preventing
Hagnosing and treating e.g. leukaemia, inflammation and immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 26912; 1399pp + Sequence Listing; English.
                                                                                                   The invention relates to isolated lung tumour-specific protheir corresponding cDNA molecules. Lung tumour-specific pertheir antigen-presenting cells are useful for stimulating expanding T cells specific for a tumour protein, and for ithe development of cancer. The invention also relates to a
                                    New human lung-specific polynucleotides and polypeptides diagnosis and treatment of disease e.g. lung cancer -
                                                                                                                                            expanding T cells specific for a tumour protein, and for the development of cancer. The invention also relates to useful for stimulating an immune response, and for treatiling tumour specific oligonucleotide is useful in gene thangousis, detection and treatment of lung cancer. The prishuman T cell epitope related to lung tumour-specific p
                                                                                                                                                                                                                                                                          Length 16
                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                       DB 22;
0.0002;
                                                                                                                                                                                                                                                                 Score 98; DB
Pred. No. 0.0
0; Mismatches
                                                                          Claim 2; Page 378; 378pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                AA013020 standard; Protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polypeptide SEQ ID NO 26912.
                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                                                                                                            35 FQANCGIDFIIFWIFW 50
                                                                                                                                                                                                                                                                                                                          18.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0515126
2000US-0577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                       Conservative
            WPI; 2001-639201/73.
                                                                                                                                                                                                                                                                        Similarity
16; Conserv
                                                                                                                                                                                                                                   16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-514838/56.
N-PSDB; AAI92951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytokine, ceil pi
production of oth
polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAY-2000;
                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                          AA013020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue
                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                     AA013020
                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The
ò
```

PR XX PA

PI XX DR

DR

PT XX XX XX CC

```
Peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 105
                                                                                                                                                                    of the printed
                                                                                                                                                                                                                                                                                                                                                                                                     65
                                                                                                                                   Note: The sequence data for this patent did not form part of the printer specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytokine; cell proliferation; cell differentiation; gene therapy; stem cell growth factor; haematopoiesis; growth factor; haematopoiesis; growth factor; immunomodulatory; cancer; leukaemia; system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                               10 SLGDSETLSQTEL---RKKERKKKRERKFQANCG-IDFIIFWIFWILLFSHHWIQESLLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                              ||||| | | : |: |||||| | || | |: |
59 SLGDRARLPQRKRERERETERKRKRERASCAFCGAITFVNMW----CQKHH---
                                                                                                                                                                                                                                                                                                                                                   30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and polypeptides, useful for preventing
7 e.g. leukaemia, inflammation and 1mmune
                                                                                                                                                                                                                                                                                                  22; Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 18532; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                      Score 82; DB 2.
                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       iagnosing and treating e.g. leukaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human polypeptide SEQ ID NO 18532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 PPSPKEVTCREMLTGGCLPWAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----LPWLT
                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                    15.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAO04640 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001WO-US04927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -TCNH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acids
                                                                                                                                                                                                                                                                                                  Similarity
28; Conserv
                                                                                                                                                                                                                                121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAI84571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-2001.
                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAO04640;
                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT,
```

Length 141;

DB 22;

Matches

SSSSSXS

AA009875 RESULT

g

ŏ

×

```
Matches
                                                                                                                                                                                                                                  RESULT 5
                                                                                                                                                                                                                                                AAG75462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DR
XX
PT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _{\rm PS}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \mathbf{PT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PI
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD
                                                                                                                                                                            Dp
                                                                                                     g
                                                                                                                                        δy
                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     form part of the printed
ormat directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    naematopolesis regulating
immunomodulatory activity and
ful in the diagnosis and/or
system disorders, arthritis and
                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
 treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
arthritis and
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English
                                                                                                                                                  46;
                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 23767; 1399pp + Sequence Listing;
                                                                                                                                                                                            Indels
                                                                                                                                                                                             5
                                                                                                                                                        Score 71.5; DB 22;
Pred. No. 0.69;
                                                                                                                                                                               Pred. No. v.v. Mismatches
                                                                                                                                                                                                                                                                                                                                                                     AAO09875 standard; Protein; 141 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polypeptide SEQ ID NO 23767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukaemia,
                                                                                                                                                                                                                                         34
                                                                                                                                                                                                                                                        SETLSQTELRKKERKKKRERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001WO-US04927
                                                                                                                                                            13.4%;
nilarity 81.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-514838/56.
N-PSDB; AAI89806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                  al Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammation.
                                                                                                                                     46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                AA009875;
                                                                                                                                       Sednence
                                                                                                                                                                       Query Match
                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
```

RX F

XX PI XX DR

PR PR

XX XX X

OS XX PN

Sequence

```
AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene cancer antigens have cytostatic activity and can be used in gene production. N and P may be used in the prevention, characters and treatment of diseases associated with decreased expression by rectifying mutations or deletions associated with decreased expression by rectifying mutations or deletions associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of P by expressing in a patient or to supplement the patients own production of P. Maditionally, N may be used to produce the colon cancer-associated Ps. Additionally, N may be used to produce the colon cancer-associated Ps. C. to express the proteins. N and P can be used in the prevention, diagnosis and AAB77789 represent sequences used in the exemplification of the present invention.

Or have an appear of the process of the sequence listing were missing at time of publication.
                              .
Μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acids encoding 4277 human colon cancer-associated polypeptides, or preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                        5 KVAVSYDLTMHSNLSNSETLSQKEKTKQTKTKQKKTYXEGRKHIKRCPTPLIIREIQIQT 64
                                                                             1 EVEVSRD---HASLGDSETLSQTELRKKERKKKRE-----RKFQANCGIDFIIFWIFWIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 163;
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human colon cancer antigen protein SEQ ID NO:6226.
                                            36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 71.5; D
Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      time of publication, meaning no 027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA;
                         2.5;
                                           Mismatches
Score 71.5;
Pred. No. 2.
                                                                                                                                                                                                                                    65 TVRYHFTHIRIVLLPOKONKCWCR 88
                                                                                                                                                                                          53 LFSHHWIQ-ESLLCPPSPKEVTCR 75
                                                                                                                                                                                                                                                                                                                                                            AAG75462 standard; Protein; 163 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.4%;
                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000WO-US26524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0157137.
99US-0163280.
     13.4%;
iilarity 31.0%;
Conservative 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-235357/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    missing at time
SEQ ID NO:1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAH34867
            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200122920-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM,
                                                             26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                        AAG75462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
```

```
2000US-0230437.
2000US-0230437.
2000US-0231242.
2000US-0231243.
2000US-0231243.
2000US-0231244.
2000US-0231413.
2000US-0231414.
2000US-0231414.
2000US-0231414.
2000US-0231414.
2000US-0231414.
2000US-0231414.
2000US-0231414.
2000US-023198.
2000US-0232397.
2000US-0232399.
2000US-0234997.
2000US-0234998.
2000US-0234997.
2000US-0234997.
2000US-0234998.
2000US-0234997.
2000US-0234997.
2000US-0234997.
2000US-0234997.
2000US-02346479.
2000US-0244617.
2000US-0244617.
2000US-0246478.
2000US-0246478.
2000US-0246478.
2000US-0246528.
2000US-0246528.
2000US-0246529.
2000US-0246529.
2000US-0246529.
2000US-0246532.
2000US-0249201.
2000US-0249213.
2000US-0249213.
2000US-0249213.
                 05-SEP-2000;

06-SEP-2000;

06-SEP-2000;

08-SEP-2000;

14-SEP-2000;

15-OCT-2000;

16-OCT-2000;

17-OCT-2000;

18-OCT-2000;

18-OCT-2000;

19-OCT-2000;

19-NOV-2000;

10-NOV-2000;

10-NOV-2000;

11-NOV-2000;

11-NOV-2000;
                    Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
                                                     47
                 Gaps
                                   9
                                  HHWIQESLLC
                                                  GHSMQAQFCC
                                                                                                                                                         1089
                                                                                                                                                         Q
             Indels
                    SLGD-SETLSQTELRKKERKKKRERKFQANCGIDFIIFWIFWILLFS
                                          SEQ ID N
            <u>.</u>
ن
                                                                                                                                         Human musculoskeletal system related polypeptide
         Mismatches
                                    5;
                                                                                      standard; Protein; 66
                                                                                                                                                                                                                                                                                                   2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0190076.
2000US-0190076.
2000US-0190076.
2000US-0209467.
2000US-0214886.
2000US-0215135.
2000US-0216847.
2000US-0216880.
2000US-0216890.
2000US-0217496.
2000US-0218290.
2000US-0218290.
2000US-0225214.
2000US-0225214.
2000US-0225266.
2000US-0225268.
2000US-0225270.
2000US-0225270.
2000US-0225270.
2000US-0225757.
2000US-0225757.
2000US-0225759.
2000US-0225759.
2000US-0225759.
2000US-0225759.
2000US-0225788.
2000US-0225788.
2000US-0225788.
2000US-0225789.
2000US-0225789.
2000US-02258924.
2000US-0229343.
2000US-0229344.
                                                                                                                                                                                                                                                                                      2001WO-US01338
                                                                                                                             entry)
    Conservative
                                 SLGDKSETLSP
                                                                                                                            (first
                                                                                                                                                                                                                                              WO200155367-A1
                                                                                                                                                                                                                                                                                                                            16-MAR-2000;

16-MAR-2000;

17-MAR-2000;

17-MAR-2000;

19-MAY-2000;

07-JUN-2000;

07-JUN-2000;

07-JUL-2000;

11-JUL-2000;

11-JUL-2000;

14-JUL-2000;

14-JUL-2000;

14-JUL-2000;

14-JUL-2000;

14-JUL-2000;

14-JUL-2000;

14-JUL-2000;

14-JUL-2000;

14-JUL-2000;

14-AUG-2000;

152-AUG-2000;

22-AUG-2000;

22-AUG-2000;

21-SEP-2000;

01-SEP-2000;

01-SEP-2000;
                                                                                                                         08-JAN-2002
                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                  17-JAN-2001;
                                                                                                                                                                                                                                                                                                     31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
                                                                                                                                                                                                                                                                 02-AUG-2001
                     10
                                                                                                      ABB03142;
                                                                                     ABB03142
Matches
                                                                         ABB031
                   δ
                                     g
                                                                                                                                                                   Π
```

vaccine

cancer;

```
cytostatic; dermatological; virucide;
                                               immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulr antiparkinsonian; antisickling; antianaemic; antiarthritic; cancerantirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal, antiparasitic; cardiant; immune disorder; cardiovascular disorder, neurological disease; infection; nephrotropic; gene therapy; vaccineurological disease;
             polypeptide SEQ ID NO
                                                                                                                                                                                                                                                                 2000US-0189659.
2000US-0184664.
2000US-0186350.
2000US-0189874.
2000US-0199076.
2000US-0198123.
2000US-0209467.
2000US-0214886.
2000US-0214886.
2000US-0216647.
2000US-0216647.
2000US-0216647.
2000US-0217487.
2000US-0217487.
2000US-0217487.
2000US-0217487.
2000US-0220964.
2000US-0225213.
2000US-0225266.
2000US-0225267.
2000US-0225267.
2000US-0225267.
2000US-0225268.
2000US-0225268.
2000US-0225267.
2000US-0225267.
2000US-0225267.
2000US-0225268.
2000US-0225268.
2000US-0225267.
2000US-0225268.
2000US-0225268.
2000US-0225268.
2000US-02252847.
2000US-02252847.
2000US-0225289.
2000US-0229343.
2000US-0229343.
2000US-0229343.
2000US-0229343.
2000US-0229343.
2000US-0229343.
2000US-0229343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0231413.
2000US-0231414.
2000US-0232080.
2000US-0232081.
2000US-0231968.
                      Human nervous system related
                                                                                                                                                                                                                                              2001WO-US01334
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 - AUG - Z000;

14 - AUG - 2000;

13 - AUG - 2000;

22 - AUG - 2000;

22 - AUG - 2000;

23 - AUG - 2000;

23 - AUG - 2000;

23 - AUG - 2000;

20 - AUG - 2000;

01 - SEP - 2000;

06 - SEP - 2000;

08 - SEP - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                              07 -JUL-2000;
07 -JUL-2000;
11 - JUL-2000;
14 - JUL-2000;
26 - JUL-2000;
26 - JUL-2000;
26 - JUL-2000;
14 - AUG-2000;
14 - AUG-2000;
14 - AUG-2000;
                                                                                                                                                                                                                                                                         31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
19-MAY-2000;
19-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                            WO200159063-A2
                                                                                                                                                                                                                                                  -JAN-2001;
                                                                                                                                                                 sapiens
                                                                                                                                                                                                                        16-AUG-2001.
 23-JAN-2002
                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PR
PR
PR
PR
PR
PR
PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PR
PR
PR
PR
PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR
PR
PR
                                                                                                                                                                                                                                                                                                                                                                  PR
PR
PR
PR
                                                                                                                                                                                                                                                                                             PR
PR
PR
PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.g. by
e of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as; (d) wound and epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ormat directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nmune haemolytic
crohn's disease,
tive colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               system useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ls, proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ovarian cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel genes (AAL34669-AAL37666) and proceed to associated with the musculoskeletal system (ABB03087-ABB04109) associated with the musculoskeletal system for preventing, treating or ameliorating medical conditions e.g. protein or gene therapy. The genes are isolated from a range of protein or gene therapy. The genes are useful in the diagnosis, treating antibodies and (ant)agonists are useful in the diagnosis, treating prevention of: (a) cancer, e.g. breast and ovarian cancer and prevention of: (a) cancer, lung, or urogenital; (b) immune cher cancers e.g. Addison's disease, allergies, autoimmune haemoly discorders e.g. Addison's disease, allergies, autoimmune haemoly cancernia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, and ilitus, Crohn's disease, correlation and lections diseases e.g. cerebral anoxia and epic healing; (e) neurological diseases e.g. cerebral anoxia and epic parasitic infections.

C parasitic infections diseases such as viral, bacterial, fungal and (f) infections diseases such as viral, bacterial, fungal and printed specification, but was obtained in electronic format disconting wipo at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                     and/or prognosing
em including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indel
                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polypeptide for treating, preventing and/or prodisorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVEVSRDHASL----GDSETLSQTELRKKERKKKRERK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; SEQ ID NO 1089; 781pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 69.5; Di
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ed. No. 1.8 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                             Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.1%;
50.0%;
    2000US-0249217.
2000US-0249218.
2000US-0249244.
2000US-0249245.
2000US-0249264.
2000US-0249264.
2000US-0249265.
2000US-0249299.
2000US-0249299.
2000US-0250391.
2000US-0251988.
2000US-025188.
2000US-0251869.
2000US-0251869.
2000US-0251869.
2000US-0251869.
2000US-0251869.
2000US-0251869.
2000US-0251989.
2000US-0251989.
                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                              Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                        2001-451937/48.
)B; AAL34724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 AA;
          17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                          11-DEC-2000;
05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB17957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB17957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis
                                                                                                                                                                                                                                                                                                                                                                  Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB17957
                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                        δ
```

PR PR PR XX XX PA YX

PR PR PR PR PR

PR PR PR PR PR PR

XX DR

```
2000US-0232397.
2000US-0232398.
2000US-0232398.
2000US-0232400.
2000US-0232401.
2000US-0233064.
2000US-0233064.
2000US-0233064.
2000US-0233065.
2000US-0234998.
2000US-0236369.
2000US-0236369.
2000US-0236369.
2000US-0246527.
2000US-0246527.
2000US-0246528.
2000US-0246529.
2000US-0249219.
2000US-0249219.
2000US-0249219.
2000US-0249218.
2000US-024929.
2000US-0249299.
14-SEP-2000;
15-SEP-2000;
16-NOV-2000;
17-NOV-2000;
18-NOV-2000;
18-NOV-2000;
18-NOV-2000;
18-NOV-2000;
19-NOV-2000;
11-NOV-2000;
11-NO
     PRARA RAGA SARA RAGA SARA
```

```
The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections.
                                                                                                                                                                                                                                                                acids encoding 3224 human nervous system antigen polypeptides, or preventing, diagnosing and/or treating nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chimera; cDNA library preparation; serotonin;
                                                                                                                                                                                                                                                                                                                  Claim 11; SEQ ID NO 6614; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VEVSRDHASL ---- GDSETLSQTELRKKERKKRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ||:| |:
VAVSQDSATTLQPGRQSKTLSQKKKKKKKKKKRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 69; DB
Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                      Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM51507 standard; Protein; 423 AA.
     2000US-0251030.

2000US-0251988.

2000US-0256719.

2000US-0251479.

2000US-0251856.

2000US-0251868.

2000US-0251869.

2000US-0251989.

2000US-0251989.

2000US-0251989.

2000US-0251989.
                                                                                                                                                                            SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.0%;
llarity 51.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse; 5HT receptor; chimer G protein-coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                            useful for preventing, cancers and metastases
                                                                                                                                                                                                 Barash SC,
                                                                                                                                                                     (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                           WPI; 2001-541565/60.
N-PSDB; ABA14283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse 5HT receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 AA;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP2001178476-A.
                                                                                                                                                                                              Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUL-2001.
                                                                                                                                                                                                                                                              Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                            PR
PR
PR
                                                                   PR
PR
PR
                                                                                                            PR
PR
PR
                                                                                                                                                                                                                                                                         XX
PT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 αq
```

1;

Wed

```
Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                        RESULT
AAE2059
                                                                                                                                                                                                                                                                                                                                                                                                XX
DT
                                                                                                                                                                                                                                                                                 g
qq
                                                                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                                                                 Qγ
                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                 5,
                                                                                                                                                                                                                                                                                                                 387
                                                                                                                                                                                                                                                                                 327
                                                                                                                                                                                                                                                                                                 87
                                                                                                        a carboxy
synthesized
                                                                                                                                                                                                                                                                                                                 PVPSFRVAWTE
                                                                                                                                                                                                                                                                                                 -PPSPKEVTCREMLTGGCLPWAT
                                                                                                                                                                                                                                                                                 SKAIHTNNALY
                                                                                                                                                                                         an orphan
                                                                                                                                                         The present sequence is provided in a specification relating to the
                                                                                                 expressing
                                                                                                                                                              preparation of a chimera cDNA library containing a cDNA encoding a functional protein. The specification describes the preparation of a serotonin-related cDNA library, and the preparation of a grotein-coupled receptor chimera cDNA library from which an orphonents
                                                                                                                                                                                                                                                                                                                                                                                                                                                          e-1-P04;
                                                                                                                                                                                                                                                  46;
                                                                                              Preparing a chimera cDNA library comprises recombinantly expcDNA with a protein translation frame and a cDNA containing terminal side from a stored region of a functional protein a
                                                                                                                                                                                                                                                                           Mouse; G-protein coupled receptor; GPCR; RP-23; sphingosin sphingosine-1-phosphate; therapy; cardiovascular disease; inflammatory disease; cell signalling.
                                                                                                                                                                                                                                                                                                                 FAFHWFAMSSICYNPFIYCWLNENFRVELKALLSMCQRPPKPQEDRLPS
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                 SLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWI---FWILL
                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                         RP-23 protein.
                                                        SANGYO GIJUTSU SOGO KEN.
                                                                                                                                                                                                                                                  41;
                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                cDNA was isolated
                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                Score 68; DB
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                         coupled receptor (GPCR)
                                                                                                                                                                                                                                        No.
                                        TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                         423 AA.
                                                                                                                                        24pp; Japanese
                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                 12.8%; 22.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Walker P
                                        SCI &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000WO-SE02563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99SE-0004660
                                                                                                                                                                                                                                                                                                                                                                                          AAE03740 standard; Protein;
        99JP-0373989
                        99JP-0373989
                                                                                                                                                                                        protein-coupled receptor protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                 Conservative
                                                        SANGYOSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB
                                                                                                                                                                                                                                                                                                 FSHHWIQESLLC-
                                        OF IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ASTR ) ASTRAZENECA
                                                                      2001-599907/68
B; AAI69851.
                                                                                                                                                                                                                                                                                                                                 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lembo P,
                                                                                                                                                                                                                                         Similarity 29; Conser
                                                                                                                                                                                                                 423 AA;
                                                                                                                                       ; 9
                                                                                                                                                                                                                                                                                                                                           :|| |||
KSH-GRR
                                                                                                                                                                                                                                                                                                                                 RSHLGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                          G-protein
                                                                                                                                        Fig
                                                KUBO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200144439-A2
                                         AGENCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-DEC-1999;
        28-DEC-1999;
                        28-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                          04-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUN-2001
                                                                                                                                       7;
                                                                                                                                                                                                                                                                 10
                                                                                                                                                                                                                                                                                                 54
                                                                                                                                                                                                                                                                                 271
                                                                                                                                                                                                                                                                                                                                 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŝ
                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                 uery Match
                                        (AGEN )
(KUBO/)
(KEIZ-)
                                                                                                                                                                                                                                         Local
                                                                                                                                         Example
                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ahmad
                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus
                                                                        WPI
                                                                                                                                                                                                                                                                                                                                                                                                                                 ID
g
                                                                                                                                                                                                                                                                                                 ď
                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                 Q
                                                                                                                                                                                                                                                                                                                                                 Db
```

```
ς,
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          387
                                                                                                                                                                                    The present sequence is mouse G-protein coupled receptor (GPCR) RP-23 protein. RP-23 is a ligand for sphingosine-1-phosphate (sphingosine-1-PO4) which is formed by the breakdown of sphingolipids and is involved in cell signalling. Sphingosine-1-PO4 causes an increase in intracellular calcium concentration. The present invention relates to methods for determining whether a test compound modulates interactions between sphingosine-1-PO4 and RP-23 a particular G-protein coupled receptor. The method is useful for determining a modulator which binds sphingosine-1-PO4 to an RP-23 receptor. The compounds identified are useful as thereapeutic agents for treating cardiovascular diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87
                                                            Determining modulator of binding of sphingosine-1-PO4 to RP-23 receptor, involves incubating sphingosine-1-PO4 and RP-23 receptor with test compound, determining the binding and comparing with a control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; G-protein coupled receptor; GPCR; transgenic animal; receptor;
genetic therapy; pharmacological; genetic disease; neuropsychological;
neurological; psychotic illness; nephrotropic; gynaecological;
pyschostimulant; glucocorticoid-induced receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAFHWFAMSSTCYNPFIYCWLNENFRVELKALLSMCQRPPKPQEDRLPSPVPSFRVAWTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --PPSPKEVTCREMLTGGCLPWAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWI---FWILL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glucocorticoid-induced receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 68; DB Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       423 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      and cancers.
                                                                                                                                                    25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-217058P.
2000US-217179P.
2000US-217223P.
2000US-217253P.
2000US-217255P.
2000US-217256P.
2000US-217257P.
2000US-217347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.8%;
22.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001WO-US21923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSHHWIQESLLC --
                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammatory diseases
                                                                 Determining modulator receptor, involves inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94
WPI; 2001-398140/42
N-PSDB; AAD08133.
                                                                                                                                                      Disclosure; Fig 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
29; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               423 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSHLGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSH-GRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200203793-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JUL-2000;
10-JUL-2000;
10-JUL-2000;
10-JUL-2000;
11-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JUL-2000;
10-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE20598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
```

```
The invention relates to a non-human transgenic animal having targetted G-protein coupled receptor (GPCR) gene disruptions in melanocortin-3 gene 5-HT-2B gene, chemokine receptor 9A gene, glucocorticoid-induced receptor gene, orphan GPR10 (UHR)-1) gene, orphan GPR14 gene, orphan GPR15 gene, beta chemokine receptor (EDI) gene, endothelial differentiation GPCR3 (EDG3) gene, ATP receptor P2UI gene or adenosine 3 receptor gene. The transgenic animal is useful for identifying an agent that ameliorates a phenotype associated with a disruption in the target gene. A transgenic construct is useful for producing a transgenic animal, an efficacy of proposed genetic and pharmacological therapies for human genetic diseases, such as neurological, neuropsychological or psychotic illnesses. The transgenic animal is also useful as models for diseases, disorders or conditions associated with phenotypes relating to a disruption in a target, and to identify pharmaceuticals, therapies, drugs and interventions which may be effective in treating a disease or other phenotypic characteristics of the animal. An agent which modulates the expression of the target gene is useful as a therapeutic for treating conditions associated with a disruption of the target gene is useful as a therapeutic for treating sequence is human glucocorticoid-induced receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87
                                                                                                                                                                                                                                                                                                                                    l non-human transgenic animal, especially transgenic mice useful
identifying an agent that modulates expression or function of
et gene, comprises disruptions in target G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAFHWFAMSSTCYNPFIYCWLNENFRVELKALLSMCQRPPKPQEDRLPSPVPSFRVAWTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEGCLPWAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAIHTNNALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGDVTTEQYLALR --- RKKKTTVKMLVLVVVLFALCWFPLNCYVLLLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --PPSPKEVTCREM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWI---FWILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 68; DB Pred. No. 22; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY28851 standard; Protein; 458 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
2000US-217537P.
2000US-218069P.
2000US-218074P.
2000US-21483P.
2000US-221483P.
2000US-223120P.
2000US-223122P.
2000US-243958P.
2000US-2499E.
2000US-262299P.
2001US-262113P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.8%;
larity 22.8%;
Conservative ]
                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 7; 101pp;
                                                                                                                                                                                                                                                        Brennan IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSHHWIQESLLC
                                                                                                                                                                                                                     (DELT-) DELTAGEN INC
                                                                                                                                                                                                                                                                                      WPI; 2002-164574/21
N-PSDB; AAD32919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 29; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        423 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|| |||
KSH-GRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSHLGRR
12-JUL-2000;
12-JUL-2000;
12-JUL-2000;
12-JUL-2000;
27-JUL-2000;
07-AUG-2000;
07-AUG-2000;
15-NOV-2000;
26-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                    target gene,
                                                                                                                                                                   16-JAN-2001;
16-JAN-2001;
                                                                                                                                                                                                                                                    Allen KD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY28851
                                                                                                                                                                                                                                                                                                                                       Novel
                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY28851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best
                                                  PR
PR
PR
PR
PR
PR
                                                                                                                                                                                                                  PA
XX
PI
                                                                                                                                                                                                                                                                                                   XX
                                                                                                                                                                                                                                                                                                                                                                                  PT
PT
PT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
```

```
The present protein sequence is the non-endogenous, constitutively active form of human 5-HT2C serotonin receptor. A point mutation replaces a Ser with Lys in the third intracellular loop of the 5-HT2C receptor. This activated receptor allows linkage to the transduction pathway and produces a biological response. This sequence can be used to identify antagonists that bind serotonin receptors and reduces the baseline intracellular response caused by receptor activation. Constitutive expression of this receptor is suitable for drug screening and to identify agents of very high specificity. These compounds are potentially useful for treating or preventing disorders involving central nervous system and cardiovascular, gastric or inflammatory disorders, that
                                                                                                                                                                                                                                  5-HT2C replaced by Lys"
                                                        Serotonin receptor; 5-hydroxytryptamine; human 5-HT2C; non-endogenous; active form; point mutation; third intracellular loop; specificity; linkage; transduction pathway; biological response; antagonist; AP-1; baseline intracellular response; compound; treatment; prevention; agent; central nervous system; cardiovascular disorder; drug screening; gastric or inflammatory disorder; constitutive expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - ERKFQANCGIDFILFWIFWILLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNTAEEENSANPNODONARRKKKERRPRGTMQAINNERKAKKVLGIVFFVFLIMWCPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liaw CW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lawless MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                serotonin receptor (AP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inverse agonists
                                                                                                                                                                                                                                  in endogenous form of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glen RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Foster RJ, Glen
JR, Thomsen WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 68;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RDHASLGDSETLSQTELRKKERKKKR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -EKSCNOKL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid, used to identify cardiovascular disease
                                                                                                                                                                                                Location/Qualifiers
310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHHWIQESLLCPPSPKEVTCREML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Fig 5b; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith JR,
                                                                                                                                                                                                                                 "Ser
                                                                                                                                                                                                                                                                                                                                              98US-0060188.
98US-0090783.
98US-0112909.
99US-0123000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.8%;
27.4%;
                              Active form of human 5-HT2C
                                                                                                                                                                                                                                                                                                                    99WO-US08168
  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              involves these receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      PHARM INC
                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chalmers DT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 ITNIL--SVLC--
(first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1999-611285/52.
B; AAZ08098.
                                                        Serotonin receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                   (AREN-) ARENA PHAR
(TRIP-) TRIPOS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
23; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             458 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Russo JF,
                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or preventing
                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                            14-APR-1998;
26-JUN-1998;
18-DEC-1998;
05-MAR-1999;
                                                                                                                                                                                                                                                           WO9952927-A1
                                                                                                                                                                                                                                                                                                                   14-APR-1999;
  25-JAN-2000
                                                                                                                                                                                                                                                                                      21-0CT-1999
                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Behan DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI
PN
XX
PD
                                                                                                                                                                                                                                                                                                                               XX
PR
                                                                                                                                                                                                                                                                                                                                                           PR
PR
XX
PA
PA
PI
PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XX
PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db
```

RESULT 12

EKSCNOKL

ITNIL--SVLC-

329

```
The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743 and AAA30775-A30779). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TW6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acids N terminal of an endogenous proline in TM6 to form a sequence X-(AA)15-Pro. The endogenous residue in IC3 at a position 16 amino acids of preferably Lys. When the endogenous residue at this or IA4, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Promacon andogenous residues. The constitutively active GPCRs are useful for identifying antagonists, agonists and partial agonists for use as the conditions. Antagonists for a particular GPCR are useful for treating diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous injudies. Sequences AAY90677 and AAY90683-Y90687 the mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --ERKFQANCGIDFIIFWIFWILLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FVFLIMWCPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G protein-coupled cuse as pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                        . bu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 458;
                                                                                                                                    G protein-coupled receptor; GPCR; constitutively active;
intracellular loop 3; transmembrane domain 6; drug screeniagonist; antagonist; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activated human (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ed. No. 24;
Mismatches
                                                                                                         G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 68;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 RDHASLGDSETLSQTELRKKERKKRR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78
AAY90676
ID AAY90676 standard; Protein; 458 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nous constitutively act:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHHWIQESLLCPPSPKEVTCREML
                                                                                                                                                                                                                                                                                                                                                                                             Liaw CW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.8%;
llarity 27.4%;
Conservative
                                                                                                                                                                                                                                                                                                    99WO-US23938
                                                                                                                                                                                                                                                                                                                                 98US-0170496
                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 297-298;
                                                                                                                                                                                                                                                                                                                                                                INC
                                                                                                                                                                                                                                                                                                                                                                                          DT,
                                                                                                                                                                                                                                                                                                                                                                                            Chalmers
                                                                                                                                                                                                                                                                                                                                                                PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                       2000-329165/28
)B; AAA30742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   458 AA;
                                                                                                                                                                                                                                          WO200022129-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Non-endogenous receptors, uses
                                                                                                                                                                                                                                                                                                                                                                ARENA
                                                                                                         Human mutant
                                                                                                                                                                                              Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                    12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                 13-OCT-1998;
                                                                                                                                                                                                                                                                       20-APR-2000.
                                                                          21-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                                                                                                                                                                                                                                          Behan DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                (AREN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                   ΚW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
```

```
This invention describes novel 1-Phenyl-3-(3-(4-bromo-3-pyrazolyl)phenyl)
-urea derivatives (I) which are modulators of non-endogenous,
constitutively activated forms of serotonin 5-HT2A (and 5-HT2C) receptors
and inverse agonists to 5-HT2A receptors. (I) modulate serotonin 5-HT(2A)
receptor activity and are potentially useful for treating central nervous
system (CNS), gastrointestinal, cardiovascular and inflammatory
                                                                                                                                  agonist;
modulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New 1-phenyl-3-(3-(4-bromo-3-pyrazolyl)phenyl)-urea derivatives, usefu as 5-HT(2A) receptor ligands e.g. for treating central nervous system, gastrointestinal, cardiovascular and inflammatory disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNTAEEENSANPNODONARRKKKERRPRGTMQAINNERKAKKVLGIVFFVFLIMMCPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --ERKFQANCGIDFIIFWIFWILLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                 Human serotonin receptor; 5-HT2A receptor; 5-HT2C receptor; agon 1-Phenyl-3-(3-(4-bromo-3-pyrazolyl)phenyl)-urea derivative; modu central nervous system disorder; CNS; gastrointestinal disorder; cardiovascular disorder; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                               Russo
Beeley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Menzaghi F,
Liaw CW,
                                                                                                         associated protein SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                           0,
'MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               Behan DP, Liu (
Glen RC, Lawless
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55-58; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 RDHASLGDSETLSQTELRKKERKKRR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - : | : |
EKSCNQKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHHWIQESLLCPPSPKEVTCREML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred
                          458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB93643 standard; Protein; 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.8%; 27.4%;
                                                                                                                                                                                                                                                                                                        98US-0112909.
99US-0123000.
99US-0152708.
99US-0292069.
99US-0292071.
                          Protein;
                                                                                                                                                                                                                                                                                 99US-0418721
                                                                               (first entry)
                                                                                                         serotonin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              DT,
                                                                                                                                                                                                                                                                                                                                                                                                      PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                              Chalmers D.
Thomsen WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITNIE--SVEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-079410/09.
N-PSDB; AAC82826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Column
                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 23; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  458 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     (AREN-) ARENA
                                                                                                                                                                                                                                                                                                        18-DEC-1998;
05-MAR-1999;
07-SEP-1999;
14-APR-1999;
14-APR-1999;
                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                 15-OCT-1999;
                                                                                                                                                                                                                             US6150393-A.
                                                                             20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                       21-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                               RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           system (Charseles)
                                                                                                                                                                                                                                                                                                                                                                                                                                           JR,
                        AAB45803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55
                                                  AAB45803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                               Foster
Smith J
                                                                                                          Human
                                                                                                                                                                                                   Homo
RESULT 13
AAB45803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT AAB9364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best
                                                                                                       П
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
```

3

54

```
se therapy and polynucleotides, il for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 to AAH13632 xemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lementary to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         full-length
AAH13628 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     particularly the 5602
n, and for the detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           defined in
                                                                                                   gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                       h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to
                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence and an oligonucleotide comprising a sequence compleme sequence and an oligonucleotide comprising a sequence compleme polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the compt the 5'-end sequence/3'-end sequence is selected from those def the specification. The primer sets can be used in antisense the in gene therapy. The primers are useful for synthesising polyn particularly full-length cDNAs. The primers are also useful for detection and/or diagnosis of the abnormality of the proteins the full-length cDNAs. The primers allow obtaining of the full cDNAs easily without any specialised methods. AAH03166 to AAH13633 to AAH18742 represent human cDNA sequences; AAH03166 to AAH13639 represent human amino acid sequences; and AAH13629 to represent oligonucleotides, all of which are used in the exemp of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the proteins encode
                                                                                                                                                                                                                                                                                                                                                                                                                     Τ;
                                                                                                 detection; diagnosis; antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                                                     aito K,
Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                       Saito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, pafull-length cDNAs defined in the specification, and/or diagnosis of the abnormality of the protefull-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                    Α,
                                                                                                                                                                                                                                                                                                                                                                                                      Hayashi K,
A, Nagai
                                                                 sequence SEQ ID NO:13140
                                                                                                                                                                                                                                                                                                                                                                                                     Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2537pp
                                                                                                                                                                                                                                                               99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                  2000EP-0116126
                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13140;
                                                                                                                                                                                                                                                                                                                                                                     (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                     Ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΩĦ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105
                                                                                                                                                                                                                                                                                                                                                                                                      Isogai
                                                                                                 primer;
                                                                 Human protein
                                                                                                                                                                                                                                                               29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ
                                                                                                                                  Homo sapiens
                                                                                                                                                               EP1074617-A2
                                                                                                                                                                                                                                  28-JUL-2000;
                                                                                                                                                                                                07-FEB-2001
                               26-JUN-2001
AAB93643;
                                                                                                                                                                                                                                                                                                                                                                                                                  တွ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                               Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                    Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                XX
PD
                                                                                                                                                                                                                                                                 PR
PR
PR
XX
                                                                                                                                                                                                                 XX
PF
                                                                                                                                                                                                                                                                                                                                                                                                                                  XX
DX
YY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PN
                                                                                                                                                                                                                                                                                                                                                                                  XX H
                                                                                                                                                                                                                                                                                                                                                                    PA
```

```
Gaps
                      5;
   105;
   Length
                       Indels
                   7;
 22;
                                                      - TRLKKKKKKKKKEKRN
                                           EVSRDHASLGDSETLSQTELRKKERKKKRERKFQAN
Score 67.5; D
Pred. No. 5.1;
9; Mismatches
                     6
12.7%;
ilarity 41.7%;
Conservative
                                                      |:: | |||||
EIAPLHTSLGDS
        l Similarity
15; Conserv
Query Match
Best Local S
Matches 15
                                          \boldsymbol{\omega}
```

73

RESULT 15 ABP00516

43

d

δ

ö

Gaps

The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27252 encode the human ORFX treating or preventing a pathology associated with an ORFX-associated disorder. In humans, and in the manufacture of a medicament for treating a capuences can be used in gene therapy. ORFX sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumnours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases and autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperiodon injury in various tissues and conditions resulting from Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; the printed ot form part of the printer format directly from WIPO Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders ö Length 81; Indels 12; sequence data for this patent did not ion, but was obtained in electronic for 23; SEQ ID NO:1014. ftp.wipo.int/pub/published_pct_sequences Score 67; DB Pred. No. 4.3; Mismatches Disclosure; SEQ ID 1014; 1037pp; English 81 Human ORFX protein sequence 12.6%; 48.3%; standard; Protein; 2001WO-US10836 2000US-206132P 2000US-228716P (first entry) reperfusion injury in var systemic cytokine damage. Conservative Leach MD; (CURA-) CURAGEN CORP. WPI; 2002-106308/14 N-PSDB; ABN16268. myasthenia gravis. . Similarity 14; Conser 81 AA; WO200192523-A2 N.B. The sequespecification, Homo sapiens. 29-MAY-2001; 30-MAY-2000; 29-AUG-2000; Shimkets RA, 06-DEC-2001. 24 - JUN - 2002 ABP00516; ABP00516 Sequence Query Match Local Matches

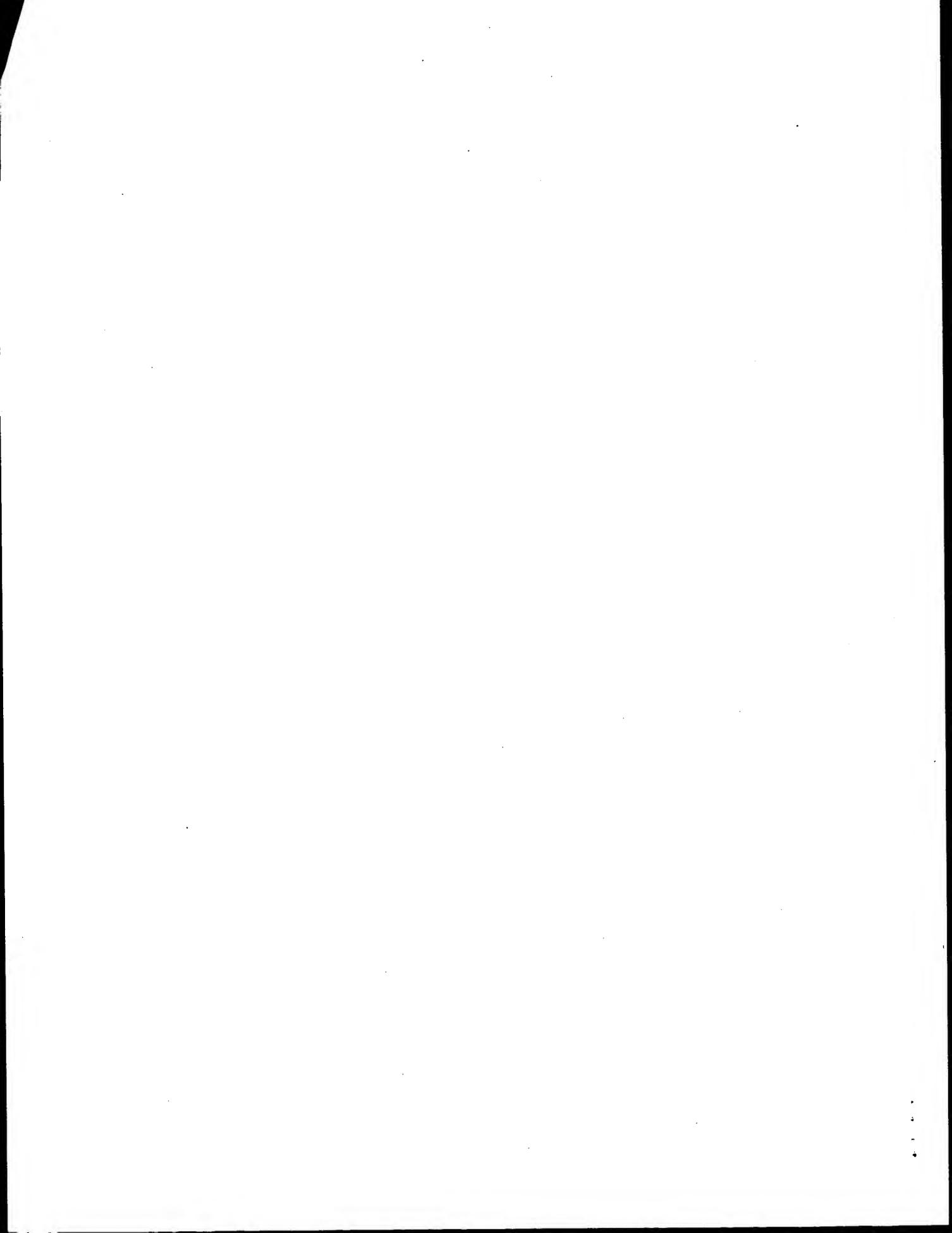
đ

Ч

Op

18 SQTELRKKERKKRERKFQANCGIDFIIF 46 | :|||| :||||| : | SHRQLRKKAKKKREARINTFCVFIFFIF 39

Search completed: July 9, 2003, 15:07:40 Job time : 56.0796 secs



```
updates/sec
                                                                                                                                      97
                                                                Search time 30.0442 Seconds (without alignments) 94.994 Million cell update:
                                                                                                                                     .....LTGGCLPWATRSHLGRRKCS
                                                                                                                                                                                                                    262574
5.1.6
Compugen Ltd
                                                                                                                                                                                                                    hits satisfying chosen parameters:
                                                                                                                                                                                            262574 seqs, 29422922 residues
version
- 2003
                                             model
                                                                   9, 2003, 15:05:28;
                                                                                                               US-09-854-133-586
532
1 EVEVSRDHASLGDSETLSQT.
                                                                                                                                                                       0
                                               S
GenCore
(c) 1993
                                                                                                                                                                       , Gapext
                                              using
                                              search,
             Copyright
                                                                                                                                                            BLOSUM62
Gapop 10.0
                                              protein
                                                                    July
                                                                                                                                                                                                                    of
                                                                                                                             score:
                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                    Total number
                                              OM protein
                                                                                                                                                                                              Searched:
                                                                                                                                        Sequence:
                                                                                                                             Perfect
                                                                      Run on:
                                                                                                                 Title:
```

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/bep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

length: 0 length: 2000000000

sed

DB DB

Minimum Maximum Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		9, Ap	9, App	, App	, Appl	7, App	, App	0, App	7, App	3, App	, App	3, App	830, A	5, App	1, App	1, App	1, App	, Appl	$\overline{}$, Appl	2, App	, Appl	_	, Appl	6, App	, Appl	2, Appli	, Appl
	Description	ednence	Sequence	Seguence	Sequence	Sednence	Sequence	Sequence	Seguence	Sednence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence	Sequence
SUMMARIES	ID	US-09-292-071-29	-09-292-069A-	S-09-767-013-2	-08-310-271-	S-09-292-071-2	-09-292-069A-	S-09-032-742-1	-09-767-013-2	S-09-292-071-3	-09-292-069A-	S-09-767-013-3	-09-134-001C-	S-09-215-694-1	-09-292-071-	09-292-069A-	S-09-767-013-3	S-08-334-773A-	08-428-24	CT-US93-1030	22-966-20	-08-157-18	-08-28	-09-450-79	-314-1	-09-450-7	-09-332-837-2	
	DB	3	₹	4	Н	m	4	4	4	ᠻ	4	4	4	4	ო	4	4		7	Ŋ	Н	7	ო	4	4	4	4	ហ
	Length	4 5	S	458	458	458	458	458	458	_	7	7	œ	œ	478	~	~	Н	Q	Q	$^{\circ}$	445	4	445	445	445	4	445
dР	Query Match	, ,	۲.	~	~	٠. د	ς.	ά.	~	ς.	α.	α.	ς.	ά.	Ή.	Ή.	Ξ.	႕	급.		1.	Ή,	Ή.	Ή.	ä	ä	-	,
	Score	89	9	68	67	67	67	29	29	99	99	99	64	64	62	62	62	H.	ŀ.	Ή.	4	Ĺ.	Ä	.	4	∺	61.5	ri.
	Result No.	t t	7	m	4	J.	9	7	80	თ	10	. 11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

328

SHHWIQESLLCPPSPKEVTCREML

55

Q

g

Sequence 71, Appl	Sequence 9, Appli	Sequence 20, Appl	Sequence 7, Appli	Sequence 7, Appli	Sequence 11, Appl	, App	Seguence 2, Appli		equence 10, Ap	, Ap	Sequence 71, Appl	Sequence 71, Appl	App.	, Ap	Sequence 11, Appl	, App	Sequence 4, Appli
-924-629C	US-09-092-636-9	-7	US-08-428-243-7	PCT-US93-10301-7	-031 - 5	US-08-194-468-2	-961-739-	US-09-514-247A-8	-5	-72	US-08-118-270-71	PCT-US93-08528-71	US-08-118-270-31	PCT-US93-08528-31	US-08-313-553-11	7-	US-07-817-920-4
4	4	4	7	2	7	٦	٣	4	4	7	1	S	Н	വ	Н	m	1
62	468	460	404	404	435		2441	44	4	160	4	4	œ	385	453	453	460
Ξ.	Ξ.	1.	4	Ξ,	11.2	Ξ.	j.	1.	1	4	-	Ή.	ŀ.	ŀ.	1.	Ή.	11.1
61	60.5	9	6	φ.	59.5	φ.	9.	9	σ,	ഹ	59	29	59	59	59	59	59
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
Sequence 29, Application US/09292071

Patent No. 6107324

GENERAL INFORMATION:

APPLICANT: Behan, Dominic

APPLICANT: Chalmers, Derick

TITLE OF INVENTION: Human Serotonin Receptors and Small Molecule Modulators

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arena Pharmaceuticals, Inc.

STREET: 6166 Nancy Ridge Drive

CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -ERKFQANCGIDFIIFWIFWILLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/292,071
FILING DATE: April 14, 1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Rosen
REGISTRATION NUMBER: 39,822
TELEPHONE: (215) 564-6525
TELEPHONE: (215) 564-6525
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.8%; Score 68; DB larity 27.4%; Pred. No. 5.5; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 RDHASLGDSETLSQTELRKKERKKRR--
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 23; Conser
                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS
                                                                                                                                                                                                                                                                                    92121
                                                                                                                                                                                                                                                    S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-292-071
RESULT 1
US-09-292-071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

ж ;

```
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                    SULT 4
-08-310-271-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                   55
                                                                                                                     Match
                                                     FEATURE:
       LENGTH:
TYPE: PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT
                                                                                                                    Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                   δy
                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-09-767-013-29

; Sequence 29, Application US/09767013
; Patent No. 6420541
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic
; APPLICANT: Chalmers, Derick
; TITLE OF INVENTION: No. 6420541-Endogenous, Constitutively Activated Human
; TITLE OF INVENTION: Serotonin Receptors and Small Molecule Modulators
; TITLE OF INVENTION: Thereo
; TITLE OF INVENTION: Thereo
; TITLE OF INVENTION: Thereo
                                                                                                                                                                                                                                                                                                               Activated Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -ERKFQANCGIDFIIFWIFWILLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6140509e1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                              APPLICANT: Liu, Qian
APPLICANT: Liu, Qian
APPLICANT: Liu, Qian
APPLICANT: Russo, Joseph F
APPLICANT: Russo, Joseph F
APPLICANT: Smith, Julian R
APPLICANT: Smith, Julian R
APPLICANT: Thomsen, William J
TITLE OF INVENTION: Serotonin Receptors And Small Molecule Mod
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
FILE REFERENCE: ARENO033
CURRENT APPLICATION NUMBER: US/09/292,069A
CURRENT FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: 60/090,783
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.8%; Score 68; DB (larity 27.4%; Pred. No. 5.5; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Thereo; TITLE OF INVENTION: Thereo; FILE REFERENCE: ARENO035; CURRENT APPLICATION NUMBER: US/09/767,013; CURRENT FILING DATE: 2001-01-23; PRIOR APPLICATION NUMBER: 09/292,072; PRIOR FILING DATE: 1999-04-14; NUMBER OF SEQ ID NOS: 33; SOFTWARE: Patentin Ver: 2.1
| :| : |
--EKSCNQKL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 RDHASLGDSETLSQTELRKKERKKKR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78
                                                                                             29, Application US/09292069A
). 6140509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               329 ITNIL--SVLC----EKSCNOKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHHWIQESLLCPPSPKEVTCREML
                                                                                                                                                                      Foster, Richaru C
Glen, Robert C
Lawless, Michael S
                                                                                                                                                        Chalmers, Derek T
Foster, Richard J
                                                                                                        Patent No. 6140509
GENERAL INFORMATION:
APPLICANT: Behan, Dominic
329 ITNIL--SVLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 23; Conserv
                                                                          US-09-292-069A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -069A-29
                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
```

```
6420541el Sequence
                                                                                                                                                                            328
                                                                                                                                               54
                                                                                                                                                                         269 RNTAEEENSANPNODONARRRKKKERRPRGTMOAINNERKAKKVLGIVFFVFLIMWCPFF
                                                                                                                                              --ERKFQANCGIDFIIFWIFWILLF
                                                                                                                Gaps
                                                                                                                18;
                                                                                4; Length 458;
                                    Sequence: No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 458;
                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 SEROTONIN
                                                                                                               28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olson and Bear
Drive 16th Floor
                                                                                                                                                                                                                                                                                                                               Patent No. 5654139
GENERAL INFORMATION:
APPLICANT: Lappalainen, Jaakko
APPLICANT: Linnoila, Markku
APPLICANT: Goldman, David
TITLE OF INVENTION: ALLELIC VARIATION OF THE
TITLE OF INVENTION: SHT2C RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
7.2;
                                                                                ore 68; DB 4 ed. No. 5.5; Mismatches
                                   Description of Artificial
                                                                                Score 68;
Pred. No.
                                                                                                                                            RDHASLGDSETLSQTELRKKERKKKR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH103.001A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67;
No.
                                                                                                                                                                                                                                     ITNIL--SVLC----EKSCNOKL 345
                                                                                                                                                                                                        78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'A:
US/08/310,271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEE: Knobbe, Martens, Olson: 620 Newport Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                         SHHWIQESLLCPPSPKEVTCREML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
JRRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,
FILING DATE:
                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08310271
Patent No. 5654139
                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fuller, Michael L
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NII
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                               12.8%;
larity 27.4%;
Conservative 15
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.6%;
27.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 619-235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                            Local Similarity
nes 23; Conser
                                ; OTHER INFORMATION:
US-09-767-013-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-310-271-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
```

d

ΩY

```
sen, William J
ON: No. 6140509-Endogenous, Constitutively Activated Human
ON: Serotonin Receptors And Small Molecule Modulators
ON: Thereof
AREN0033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --ERKFQANCGIDFIIFWIFWILLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        6140509el
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                            .
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Christina C.
N: Constitutively Activated Serotonin
N: Receptors
ES: 25
                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 67; DB 4
Pred. No. 7.2;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suite 103
                                                                                                                                                     FILE REFERENCE: ARENO033
CURRENT APPLICATION NUMBER: US/09/292,069A
CURRENT FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: 60/090,783
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/112,909
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1999-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---EKSCNOKL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 RDHASLGDSETLSQTELRKKERKKKR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/09/032,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Katharine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 SHHWIQESLLCPPSPKEVTCREML 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEE: Laurence Weinberger: 882 S. Matlack Street, P.O. Box 1663
West Chester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-032-742-10; Sequence 10, Application US/09032742; Patent No. 6255089; GENERAL INFORMATION:
APPLICANT: Teitler, Milt
APPLICANT: Herrick-Davis, Kathar; APPLICANT: Egan, Christing C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weinberger, Laurence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.6%;
nilarity 27.4%;
Conservative 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRENT APPLICATION APPLICATION NUMBER: US/098 FILING DATE: 27-FEB-1998
                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
             ഗ
                                                        Russo, Joseph F
Smith, Julian R
Thomsen, William
           Lawless, Michael
Liaw, Chen W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Cons
TITLE OF INVENTION: Cons
TITLE OF INVENTION: Rece
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Laurence We
STREET: 882 S. Matlack
STREET: P.O. Box 1663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : |:||
329 ITNIL--SVLC--
                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 3. SOFTWARE: Patentin Ver.
Robert
                  لم.
Liaw, در.
Qian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 19380-0053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE MEDIUM TYPE: F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                           APPLICANT: Russo, Jo
APPLICANT: Smith, Ju
APPLICANT: Thomsen,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-292-069A-27
                                                                                                                                                                                                                                                                                                                                 ID NO 27
ENGTH: 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME:
                           APPLICANT
                                                APPLICANT
                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qγ
                                                                                                                                                                                                                                                              APPLICANT: Behan, Dominic
APPLICANT: Chalmers, Derick
TITLE OF INVENTION: No. 6107324-Endogenous, Constitutively Activated
TITLE OF INVENTION: Human Serotonin Receptors and Small Molecule Modulators Therec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54
                                                      269 RNTAEEENSANPNODONARRKKKERRPRGTMOAINNERKASKVLGIVFFVFLIMWCPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -ERKFQANCGIDFIIFWIFWILLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                   --ERKFQANCGIDFIIFWIFWILLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
       29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.6%; Score 67; DB 27.4%; Pred. No. 7.2; tive 14; Mismatches
        Mismatches
                                                                                                                                                                                                                                                                                                                                                          E: Arena Pharmaceuticals, Inc
6166 Nancy Ridge Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 RDHASLGDSETLSQTELRKKERKKKR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78
                                        6 RDHASLGDSETLSQTELRKKERKKR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/09/292,071
4, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27, Application US/09292069A Patent No. 6140509 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHHWIQESLLCPPSPKEVTCREML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible (YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---EKSCNOKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION NUMBER: 39,822
TELEPHONE: (215) 564-6525
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acids
STRANDENTED
                                                                                                      55 SHHWIQESLLCPPSPKEVTCREML
                                                                                                                                   -- EKSCNOKL
                                                                                                                                                                                                              Sequence 27, Application US/09292071 Patent No. 6107324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
         14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Behan, Dominic E
Chalmers, Derek
Foster, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  April 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: April 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Mark J. Rosen
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITNIL--SVLC--
                                                                                                                       :: |:||
329 ITNIL--SVLC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                          San Diego
                                                                                                                                                                                                                                Patent No. 6107324
GENERAL INFORMATION:
APPLICANT: Behan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE:
US-09-292-071-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-292-069A-27
                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                    RESULT 5
US-09-292-071-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
          23;
                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                           CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                       q
```

т Ж

54

H

```
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Activated Human
                                                                                                                                                                                                                                                                                                                           269 RNTAEEENSANPNODONARRKKKERRPRGTMOAINNERKASKVLGIVFFVFLIMWCPFF
                                                                                                                                                                                                                                                                                                      --ERKFQANCGIDFIIFWIFWILLF
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Behan, Dominic

APPLICANT: Chalmers, Derick

TITLE OF INVENTION: No. 6420541-Endogenous, Constitutively Activated Hu

TITLE OF INVENTION: Serotonin Receptors and Small Molecule Modulators

TITLE OF INVENTION: Thereo

FILE REFERENCE: AREN0035

CURRENT APPLICATION NUMBER: US/09/767,013

CURRENT FILING DATE: 2001-01-23

PRIOR FILING DATE: 1999-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNTAEEENSANPNODONARRKKKERRPRGTMOAINNERKASKVLGIVFFVFLIMWCPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - ERKFQANCGIDFIIFWIFWILLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6420541el
                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                         Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.6%; Score 67; DB 4; Length 458; larity 27.4%; Pred. No. 7.2; Conservative 14; Mismatches 29; Indels
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: No. US-09-767-013-27
                                                                                                                                                                                                                                                                      29;
                                                                                                                                                                                                                                      ore 67; DB 4;
ed. No. 7.2;
Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-292-071-33

US-09-292-071-33

Sequence 33, Application US/09292071

Patent No. 6107324

GENERAL INFORMATION:
APPLICANT: Behan, Dominic
APPLICANT: Chalmers, Derick
TITLE OF INVENTION: No. 6107324-Endogenous,
                                                                                                                                                                                                                                  12.6%; Score 67; Similarity 27.4%; Pred. No. 3; Conservative 14; Mismatc
                                                                                                                                                                                                                                                                                             6 RDHASLGDSETLSQTELRKKERKKKR--
                                                                                                                                                                                                                                                                                                                                                                               329 ITNIL--SVLC-----EKSCNQKL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 RDHASLGDSETLSQTELRKKERKKKR---
                   3086-4
                                                                                                                                                                                                                                                                                                                                                               55 SHHWIQESLLCPPSPKEVTCREML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27, Application US/09767013
Patent No. 6420541
           REFERENCE/DOCKET NUMBER: 3086
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 431-1703
TELEFAX: (610) 431-4181
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 ITNIL--SVLC----EKSCNQKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHHWIQESLLCPPSPKEVTCREML
   27,965
                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                458 amino acids amino acids
                                                                                                                                                                  not relevant
                                                                                                                                                                                    protein
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 23; Conser
                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                               ; MOLECULE TYPE:
US-09-032-742-10
                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -09-767-013-27
                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO 27
TH: 458
                                                                                                                 LENGTH:
                                                                                                                                                                                                                                Match
                                                                                                                                                                                                                 Query Mac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55
                                                                                                                                 TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                           QQ
                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
```

Activated

Constitutively

```
Small Molecule Modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Constitutively Activated Human
Small Molecule Modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -ERKFQANCGIDFIIFWIFWILLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
   Human Serotonin Receptors and
                                                                                                                                                                                Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 66; DB
Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thomsen, William J
Thomsen, William J
TENTION: No. 6140509 Endogenous,
TENTION: Serotonin Receptors And
TENTION: Thereof
                                              Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RENT APPLICATION NUMBER: US/09/292,069A
RENT FILING DATE: 1999-04-14

OR APPLICATION NUMBER: 60/090,783

OR FILING DATE: 1998-06-26

OR APPLICATION NUMBER: 60/112,909

OR FILING DATE: 1998-12-18

OR FILING DATE: 1999-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHHWIQESLLCPPSPKEVTCREMLTGGCL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --CNEDVIGALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 RDHASLGDSETLSQTELRKKERKKKR---
TITLE OF INVENTION: Human Serotonin
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arena Pharmaceuticals,
STREET: 6166 Nancy Ridge Drive
                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/292,071
FILING DATE: April 14, 1999
CLASSIFICATION:
                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33, Application US/09292069A Patent No. 6140509
                                                                                                                                                                                                                                                        NAME: Mark J. Rosen
REGISTRATION NUMBER: 39,822
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                  (215) 564-6525
215) 568-3439
SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.4%;
25.8%;
                                                                                                                                                                                                                                              'AGENT INFORMATION:
Mark J. Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Foster, Richard Glen, Robert C Lawless, Michael Fiaw, Chen W
                                                                                                                                                                                                                                                                                                                                                       478 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Behan, Dominion
Chalmers, Derek T
                                                                                                                                                                                                                                                                                                                                                                                              not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    349 ITNIM--AVICKES--
                                                                                                                                                                                                                                                                                                             TELEFAX: (215) 568-34 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Russo, Joseph
Smith, Julian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liaw, Ch.
'''. Qian
                                                                   San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6140509
GENERAL INFORMATION:
APPLICANT: Behan, Do.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF INVENTION:
OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S OF INVENTION:
REFERENCE: AR
                                                                                               USA
                                                                                                                                                                                                                                              ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS
                                                                                         COUNTRY: US
                                                                                 CA
                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-292-069A-33
                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-292-071-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                 CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
TITLE OF IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
```

Jul

```
STAPHYLOCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sednence
                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Activated Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- ERKFQANCGIDFIIFWIFWILLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 RNTAEEENSANPNODONARRKKKERRPRGTMOAINNERKAKKVLGIVFFVFLIMWCPFF
                                                                                                                                                                                                                                                                         FIIFWIFWILLF
                                                                                                                                                                                                                                                                                                        289 RNTAEEENSANPNODONARRKKKERRPRGTMQAINNERKAKKVLGIVFFVFLIMWCPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modulators
                                                                                                                            6140509el
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  οĮ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6420541el
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3830, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 33, Application US/09767013

Fatent No. 6420541

GENERAL INFORMATION:

APPLICANT: Behan, Dominic

APPLICANT: Chalmers, Derick

TITLE OF INVENTION: No. 6420541-Endogenous, Constitutively Acti

TITLE OF INVENTION: Thereo

TITLE OF INVENTION: Thereo

FILE REFERENCE: AREN0035

CURRENT APPLICATION NUMBER: US/09/767,013

CURRENT FILING DATE: 2001-01-23

PRIOR APPLICATION NUMBER: 09/292,072

PRIOR FILING DATE: 1999-04-14

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1
                                                                                                                            S<sub>N</sub>
                                                                                                                                                                                                 478
                                                                                                                                                                                                                                                                       -ERKFQANCGID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence: No.
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                  Length
                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                               ore 66; DB 4;
ed. No. 9.8;
Mismatches 3:
                                                                                                                           Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.4%; Score 66; DB ilarity 25.8%; Pred. No. 9.8; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           ----CNEDVIGALL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- CNEDVIGALL 370
                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
                                                                                                                                                                                               Score 66;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 RDHASLGDSETLSQTELRKKERKKKR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 SHHWIQESLLCPPSPKEVTCREMLTGGCL
                                                                                                                                                                                                                                                                                                                                         55 SHHWIQESLLCPPSPKEVTCREMLTGGCL
                                                                                                                                                                                                                                                                     6 RDHASLGDSETLSQTELRKKERKKRR-
                                                LENGTH: 478

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of

OTHER INFORMATION: Sequence

US-09-292-069A-33
                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                             12.4%;
ilarity 25.8%;
Conservative 1
                  C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 ITNIM--AVICKES-
                                                                                                                                                                                                                                                                                                                                                               349 ITNIM--AVICKES
NUMBER OF SEQ ID NOS: 3:
SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 23; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-09-134-001C-3830
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-09-767-013-33
                                 ) ID NO 33
LENGTH: 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-767-013-33
                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O ID NO 33
LENGTH: 478
                                                                                                                                                                                               Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Д
                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>B</u>
                                                                                                                                                                                                                                                                     δ
```

```
Sequence 31, Application US/09292071
Patent No. 6107324
GENERAL INFORMATION:
APPLICANT: Behan, Dominic
APPLICANT: Chalmers, Derick
TITLE OF INVENTION: No. 6107324-Endogenous, Constitutively Activated
TITLE OF INVENTION: Human Serotonin Receptors and Small Molecule Modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3
                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --TLSQTELRKKERKKKRERKFQANCGIDFIIFWIFWILLFSHHWIQESLLCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -STCLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGENT
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/09215694B

Sequence 15, Application US/09215694B

Patent No. 6391583

GENERAL INFORMATION:

APPLICANT: Wisconsin Alumni Research Foundation

APPLICANT: Hutchinson, Charles R.

APPLICANT: Kennedy, Jonathan n.m.i

APPLICANT: Kennedy, Jonathan n.m.i

TITLE OF INVENTION: METHOD OF PRODUCING ANTIHYPERCHOLESTEROLEMIC AGEI

FILE REFERENCE: 960296.95718

CURRENT APPLICATION NUMBER: US/09/215,694B

CURRENT FILING DATE: 1999-12-18

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 15

LENGTH: 488
                                                                                                                                                                                                              ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                40 GSDFSTGWIFYIDEEGHHDLVSSVDLPEALSKNHCYYLTNGSC--WCVQAY
                                                                                                                                                                                                                                              GIDFIIFWIFWILLFSHHWIQESLLCPPSPKEVTCREMLTGGCLPWATRSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                              25;
                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                            Score 64; DB 4
Pred. No. 13;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 64; DB Pred. No. 17; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inc
                               60/055,779
60/064,964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEE: Arena Pharmaceuticals,
: 6166 Nancy Ridge Drive
San Diego
                                                                                                                             ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       th 12.0%; Sc
Similarity 26.6%; Pr
17; Conservative 13;
                                                                                                                                                                                                              6
                                                                                                                                                                             12.0%;
29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Aspergillus terreus US-09-215-694-15
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33
                                                           NUMBER OF SEQ ID NOS: 5674
EQ ID NO 3830
LENGTH: 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                         l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDSE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|:
59 AAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                            RESULT 13
US-09-215-694-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-292-071-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
CITY: S
STATE:
                                                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                            TYPE: PRT
                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QΫ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
```

```
ж;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 RNTAEEENSANPNODONARRKKKERRPRGTMQAINNERKASKVLGIVFFLFVVMWCPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIFWIFWILLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6140509el
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Activated
Modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - ERKFQANCGIDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Constitutively
Small Molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Sequence
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/292,071
FILING DATE: April 14, 1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ж
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Foster, Richard J
Glen, Robert C
Lawless, Michael S
Liaw, Chen W
Liu, Qian
Russo, Joseph F
Smith, Julian R
Thomsen, William J
INVENTION: Serotonin Receptors And Sminy Thereof
RUST ARENO033
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 62; DB 3
Pred. No. 29;
(6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CHAIMELS, DEFER TO APPLICANT: Foster, Richard JAPPLICANT: Glen, Robert CAPPLICANT: Lawless, Michael SAPPLICANT: Liaw, Chen WAPPLICANT: Liu, Qian APPLICANT: Liu, Qian APPLICANT: Smith, Julian RAPPLICANT: Smith, Julian RAPPLICANT: Thomsen, William JAPPLICANT: Thomsen, William JAPPLICANT: Thomsen, William JAPPLICANT: Thomsen, William JAPPLICANT: Thomsen, William JAPPLICANTION: NO. 6140509-Endogenous, TITLE OF INVENTION: Serotonin Receptors And TITLE OF INVENTION: Thereof FILE REFERENCE: ARENO033
CURRENT FILING DATE: 1999-04-14
PRIOR FILING DATE: 1999-06-26
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1999-03-05
PRIOR FILING DATE: 1999-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -CNEDVIGALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 SHHWIQESLLCPPSPKEVTCREMLTGGCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 RDHASLGDSETLSQTELRKKERKKR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 31, Application US/09292069A
Patent No. 6140509
                                                                                                                                                               TELECOMMUNICATION NUMBER: 39,822

TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 564-6525

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS:
TYPE: not relevant
MOLECULE TYPE: protein
US-09-292-071-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             11.78; 24.78;
                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Rosen
REGISTRATION NUMBER: 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Behan, Dominic P
Chalmers, Derek T
Foster, Richard J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         349 ITNIM--AVICKES---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 3 SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                . Similarity 22; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Behan, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-09-292-069A-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 31
LENGIH: 478
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER
US-09-292-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <del>a</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
```

```
ä
                                                                            348
                                                                  -ERKFQANCGIDFIIFWIFWILLF
                           18;
th 11.7%; Score 62; DB 4; Length 478; Similarity 24.7%; Pred. No. 29; 22; Conservative 16; Mismatches 33; Indels
                                                                                                     83
                                                                                                      SHHWIQESLLCPPSPKEVTCREMLTGGCL
                                                    6 RDHASLGDSETLSQTELRKKERKKKR--
 Query Match
Best Local S
Matches 22
                                                                                                     52
                                                                             Ωp
                                                                                                      Qγ
                                                     ò
```

9, 2003, 15:08:26

349 ITNIM--AVICKES----CNEDVIGALL 370

g

Search completed: July Job time: 35.0443 secs

```
Compugen Ltd
5.1.6
version - 2003
GenCore
Copyright (c) 1993
```

protein search, using sw model OM protein

updates/sec econds Search time 32.6195 Se (without alignments) 346.196 Million cell 2003, 15:06:38; o, July Run on:

US-09-854-133-586 532 score: Title: Perfect

EVEVSRDHASLGDSETLSQT... Sequence:

97

..LTGGCLPWATRSHLGRRKCS

Gapext BLOSUM62 Gapop 10.0 Scoring table:

0.5

445758 seqs, 116419773 residues Searched: 445758 of hits satisfying chosen parameters: Total number

seq length: 0 seq length: 200000000 DB Minimum DB Maximum

100% 45 summaries Post-processing: Minimum Match 0% Maximum Match Listing first

Database

Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*

to have a being printed of results predicted by chance to had to the score of the result being sis of the total score distribution. greater than or equal to derived by analysis of the number 18 and is score

SUMMARIES

	Description	Sequence 586, App		e 586	713	7 6	287	Sequence 587, App	Sequence 587, App	Segmence 400, App		400,	∢.,	Sequence 1089, Ap	1 Ann	100	62	_	Sequence 16, Appl	0 7	\$ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	ر ح	3, App	Sequence 291, App	
	_	HS-09-854-133-586	-10-144-649A-58		02-03-130-30 (US-10-144-649A-7	US-09-854-133-587	HS-10-144-649A-5	n me-09-738-973-		04-1/8-268-60-50	US-09-948-783-400	US-10-106-698-6236	110-00-7	02-03-04-07-00	US-09-903-396A-2	US-10-251-385-23	US-10-251-385-126	116-10-2	11.00 C77 OT CO	US-09-862-027-4	US-09-764-891-4290	0 US-09-838-622-3	rre-10-157-031-291	TOO 20T_0T_
	Length DB		100	,,	_	4	16		16	, ,	o,	119 9		, ,	٥	423 9	458 9	α) C	0		4	69	100	•
æ	Query Match Le	1 0		•	90	00	2 0	. a	•		'n		. ~	•	'n	N.	~		i	v	O	C	12.4	1 (12.4
	Score	1 (3 (232	ന	(~) 0	0 0		ת	0	80.5	· > -	- (5	99	2	200	> t	9	29	עע ע) (99
	Result No.		- 4 (7	m	7	יע	n 4	01	_	6 0	σ	, (O T	 	12	1 6) -	7	15	16	17	\ r) 	19

RESULT 2
US-10-144-649A-586
Sequence 586, Application US/10144649A
Publication No. US20030118599A1
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.

Sequence 673, App Sequence 24, Appl	Sequence 38925	6 3/340,	equence 41, APP	equence 33, Ap	744 777 744 71	Sequence 10, Apr	equence 40, App	/1, APP	equence 4, Appi	ednence	43, App	Sequence 1124,	equence 1, Appl	equence 3, App	s, Appl	equence /, Appl	equence 9, Appl	equence 11,	equence 13, Ap	, Ap	•	equence 21, Ap	odijence 23. Ap	
3 9 US-09-866-050A-6 7 10 US-09-801-368-2	US-10-001-83/-1 US-09-864-761-	7 10 US-09-864-761-3754	2 9 US-09-877-843-	5 9 US-09-877-843-39	5 9 US-10-225-567A-	1 10 US-09-989-861-1) 9 US-09-877-843-4	9 US-09-883-34	41 9 US-10-242-	09 9 US-10-06	48 9 US-	51 10 US-09-764-8	59 9 US-10-280-85	59 9 US-10-280-858-	59 9 US-10-280-85	59 9 US-10-280-858-	59 9 US-10-280-858-	59 9 US-10-280-858-1	59 9 US-10-280-85	FO 0 TIS-10-280-858-1	0 0 11C-10-280-858-1	9 9 03-10-20 030 #	2 0C0-007-0T-SO 6 6	2-858-087-10-580-6 6
4.5 12.1 1 64 12.0 4	63.5 11.9	61.5 11.6	61:5 11.6 4	61.5 11.6 4	61.5 11.	61.5 11.	61.5 11.	61 11.	7 LT LZ	0. 1. 2 3 5 5 5 5 5 5.	500.5	60.50	71.3	700	60 11	60 11.3	60	71.13	000	C: TT 00	2 60 11.3	3 60 11.3	4 60 11	5 60 11

ALIGNMENTS

```
Gaps
US-09-854-133-586

US-09-854-133-586

Sequence 586, Application US/09854133

Publication No. US20020183499A1

GENERAL INFORMATION:

APPLICANT: Lodes, Michael J.

APPLICANT: Mohamath, Raodoh

APPLICANT: Henderson, Robert A.

APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Le-48; 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 532; D
Pred. No. 1e-
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens US-09-854-133-586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity
97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QΫ
```

ö

```
1 EVEVSRDHASLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWIFWILLFSHHWIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVEVSRDHASLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWIFWILLFSHHWIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                              CANCER
                                                                                                                                                                                                                                   97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97;
APPLICANT: Algate, Paul A.

APPLICANT: Algate, Paul A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CAN

FILE REFERENCE: 210121.475C11

CURRENT APPLICATION NUMBER: US/10/144,649A

CURRENT FILING DATE: 2002-08-21

NUMBER OF SEQ ID NOS: 749

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 97

TYDE.
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                     97
                                                                                                                                                                                                                                                                                                                                                             97
                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                             Score 532; DB 9
Pred. No. 1e-48;
                                                                                                                                                                                                                                                                                                                                        61 ESLLCPPSPKEVTCREMLTGGCLPWATRSHLGRRKCS
                                                                                                                                                                                                                                                                                                                            ESLLCPPSPKEVTCREMLTGGCLPWATRSHLGRRKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 532; DB 10
Pred. No. 1e-48;
); Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESLLCPPSPKEVTCREMLTGGCLPWATRSHLGRRKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 210121.475C9
CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 586, Application US/09738973
Patent No. US20020110563A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yoseph
                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                           100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reed, Steven G.
Henderson, Robert Lodes, Michael J.
Fling, Steven P.
Mohamath, Raodoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Algate, Paul A.
Secrist, Heather
Indirias, Carol Yo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mannion, Jane APPLICANT: Kalos, Michael D. TITLE OF INVENTION: COMPOSIT TITLE OF INVENTION: THE THEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Benson, Darin R.
Elliot, Mark
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                      ; ORGANISM: Homo sapiens US-10-144-649A-586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                      Similarity 97; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Reed, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                        SULT 3
-09-738-973-586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: HOMO
US-09-738-973-586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO 586
                                                                                                                                                                         PRT
                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q
```

```
Gaps
                                                                       APPLICANT: Lodes, Michael J.
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C11
CURRENT APPLICATION NUMBER: US/10/144,649A
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 749
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                             Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF L.
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                     Score 532; DB 9;
Pred. No. 1.2e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9; Le
0.00064;
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 98;
Pred. No.
                                Application US/10144649A
b. US20030118599A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
US-10-144-649A-587
; Sequence 587, Application US/10144649A
; Publication No. US20030118599A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 587, Application US/09854133 Publication No. US20020183499A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.48; 50
100.08; P_{J}
                                                                                                                                                                                                                                                                                                                                                                                   100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 FQANCGIDFIIFWIFW 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FQANCGIDFILFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lodes, Michael J
APPLICANT: Mohamath, Raodo
APPLICANT: Henderson, Robe
APPLICANT: Benson, Darin R
APPLICANT: Secrist, Heathe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-144-649A-742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
US-09-854-133-587
                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 97; Conserv
                              Sequence 742, Application No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Similarity
16; Conserv
              -10-144-649A-742
                                                                                                                                                                                                                                                              SOFTWARE: Fas
SEQ ID NO 742
LENGTH: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-854-133-587
                                                                                                                                                                                                                                                                                                                  PRT
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

ö

ö

```
Query Match
                                                                                               PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR
PRIOR
PRIOR
                                                                                                                       FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR
                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR
                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR
                                                                                                                                                                                                                                                                                                                                             рp
                                                                                                                                                                                                                                                                                                                                                                                            Д
                                                                                                                                                                                                                                                                                                                                                                      δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                              APPLICANT: Algate, Paul A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCE
                                                                                                                                                                                                                  Length 16;
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 98; DB 10; I
Pred. No. 0.00064;
0; Mismatches 0;
                                                                                                                                                                                                               Score 98; DB 9; Le
Pred. No. 0.00064;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                            FILE REFERENCE: 210121.475C11
CURRENT APPLICATION NUMBER: US/10/144,649A
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 749
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                    Score 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 400, Application US/09892877 Publication No. US20030077809A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              Sequence 587, Application US/09738973 Patent No. US20020110563A1 GENERAL INFORMATION: APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yoseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                             18.4%; 500
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.4%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FQANCGIDFIIFWIFW 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210121.47509
                                                                                                                                                                                                                                                                     35 FQANCGIDFIIFWIFW 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Algate, Paul A.
Secrist, Heather
Indirias, Carol Y.
Benson, Darin R.
Elliot, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CANT: Mannion, Jane
CANT: Kalos, Michael D.
OF INVENTION: COMPOSIT
OF INVENTION: THE THER
                                                                                                                                                                                                                                                                                                                                                                                                         Henderson, Robert
Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Raodoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  Steven P
                                                                                                                                                                                                                                                                                   1 FQANCGIDFIFWIFW
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al 97
APPLICANT: Lodes, Michael C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-738-973-587
                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben et.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mohamath,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                           Liqun
                                                                                                                                                                                                                                  l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    Fling,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-892-877-400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                  Wang,
                             Fan,
                                                                                                                                                                                                US-10-144-649A-587
                                                                                                                                                                                                                                                                                                                                                US-09-738-973-587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCETWART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                          NUMBER
SOFTWARE: Fas
SEQ ID NO 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                         Query Match
                             APPLICANT:
                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best
                                                                                                                                                                                                                                                                                                                                      RESULT
```

qq

ò

Q

d

```
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVEVSRDHASL----GDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWIFWILLFSH 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
                                                                                                                                                                                                                                   NAME/KEY: SITE
LOCATION: (46)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
FILE REFERENCE: PZ028P1
CURRENT APPLICATION NUMBER: US/09/892,877
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658
PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 461
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----KKEKKYVLNA--TFLNFYF
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 HWIQESLLCPPSPKEVTCREMLTGGCLPWA-----TRSHLGRRKC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 400, Application US/09948783
Publication No. US20030100051A1
GENERAL INFORMATION:
APPLICANT: Ruben et. al.
TITLE OF INVENTION: 97 Human secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ed. No. 0.37;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 80.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/948,783 CURRENT FILING DATE: 2001-09-10 PRIOR APPLICATION NUMBER: 60/231,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER: PCT/US99/09847
1999-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R FILING DATE: 1998-05-12
R APPLICATION NUMBER: 60/085,927
R FILING DATE: 1998-05-18
R FILING DATE: 1998-05-18
R APPLICATION NUMBER: 60/085 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DR FILING DATE: 2000-09-11
DR APPLICATION NUMBER: 09/892,877
DR FILING DATE: 2001-06-28
DR APPLICATION NUMBER: 09/437,658
DR FILING DATE: 1999-11-10
DR APPLICATION NUMBER: PCT/US99/098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 EVAVSRDHTIALQXGGQSKXLSQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1998-05-18
APPLICATION NUMBER: 60/085,923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60/085,921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/085,924
FILING DATE: 1998-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60/085,922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TUMBER: 60/085,094
1998-05-12
NUMBER: 60/085,105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60/085,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/0
FILING DATE: 1998-05-18
APPLICATION NUMBER: 60/0
FILING DATE: 1998-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1998-05-12
APPLICATION NUMBER: 60/(
FILING DATE: 1998-05-12
APPLICATION NUMBER: 60/(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1998-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                               15.1%;
ilarity 27.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R FILING DATE: 1999-05-
R APPLICATION NUMBER: (
R FILING DATE: 1998-05-
R APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1998-0: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: 97 FFILE REFERENCE: PZ028P2
                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: SITE LOCATION: (110)
                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-09-948-783-400
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Str. 29;
                                                                                                                                                     ID NO 400
```

ъ,

72

.; ?

Gaps

7;

Indels

7;

Length 66;

DB 10;

```
328 FAFHWFAMSSTCYNPFIYCWLNENFRVELKALLSMCQRPPKPQEDRLPSPVPSFRVAWTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09903396A
Publication No. US20020184657A1
GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
TITLE OF INVENTION: GLUCOCORTICOID-INDUCED RECEPTOR GENE DISRUPTIONS
FILE REFERENCE: R-359
                         Sequence 1089, Application US/09764877
Patent No. US20020147140A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 SLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWI---FWILL-
                                                                                                                                                                                                                                                                                                                                                1 EVEVSRDHASL----GDSETLSQTELRKKERKKKRERK 34
                                                                                                                                                                                                                                                                                                                                                                     13.1%; Score 69.5; Di
50.0%; Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/903,396A
CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/217,179
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/262,205
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.8%; Score 68; DB 22.8%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF SEQ ID NOS: 4

RE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-251-385-230
; Sequence 230, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                     Similarity 50.0
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSHHWIQESLLC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                        CRGANISM: Homo sapiens
US-09-764-877-1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388 KSH-GRR 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 RSHLGRR 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
29; Conserv
                                                                                                                                                                                               NO 1089
                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-09-903-396A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-903-396A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2
LENGTH: 423
                                                                                                                                                                                                                             PRT
                                                                                                                                                                                                                                                                                      Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE
                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           αq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ruben et al.
TITLE OF INVENTION:
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                            occurring L-amino acids
                                                                                                                                                                                                                                                                                                           ng L-amino acids
                                                                                                                                                                                                                                                                                                                                                    occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVEVSRDHASL ---- GDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWIFWILLFSH 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 SLGD-SETLSQTELRKKERKKRERKFQANCGIDFIIFWIFWILLFSHHWIQESLLC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -WIAW--LYSGHSMQAQFCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HWIQESLLCPPSPKEVTCREMLTGGCLPWA----TRSHLGRRKC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -CRDKVLLCCPGWSHIVGLKQSSHLGLRKC 10
                                                                                                                                                                                                                                                                                                                                                                                                Length 11
                                                                                                                                                                                                                                                                                                         occurri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 163
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                    of the naturally
                                                                                                                                                                                                                                                                                                  NAME/KEY: SITE
LOCATION: (110)
OTHER INFORMATION: Xaa equals any of the naturally
                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Xaa equals any of the naturally
                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                          DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                                                                                       Score 80.5; DB
Pred. No. 0.37;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ed. No. 4.5;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 71.5;
Pred. No. 4
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,925
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,928
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 465
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MDEL...
2002-03-27
MER: PCT/US00/26524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60/157,137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60/163,280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-106-698-6236
; Sequence 6236, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 EVAVSRDHTIALQXGGQSKXLSQ--
                                                                                                                                                                                                                                  LOCATION: (46)
OTHER INFORMATION: Xaa equals any
NAME/KEY: SITE
LOCATION: (52)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 SLGDKSETLSP----KKKKKKKKN--
                                                                                                                                                                                                                                                                                                                                                                                                                  9;
                                                                                                                                                                                                                                                                                                                                                                                     15.18; 27.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2000-09-28
APPLICATION NUMBER: US (
FILING DATE: 1999-09-29
APPLICATION NUMBER: US (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.4%;
Llarity 38.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 22; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                               NAME/KEY: SITE
LOCATION: (46)
                                                                                                                                                                                                                                                                                                                                              US-09-948-783-400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -10-106-698-6236
                                                                                                                                       O ID NO 400
LENGTH: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-09-764-877-1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ID NO 6236
                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73
                                                                                                                                                                                                                                                                                                                                                                                               Loca1
                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR
PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                            Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
```

5

Gaps

46;

Indels

41;

DB 9; Length 423;

327

--PPSPKEVTCREMLTGGCLPWAT 87

```
Search completed: July Job time: 33.6195 secs
                                                                                                                                                                                                                                                                      US-10-225-567A-16
                                                                                                                                                                                                    SEQ ID NO 16
LENGTH: 458
                                                                                                                                                                                                                                     TYPE: PRT ORGANISM:
                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                             Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ys-quence 126, Application US/10251385

yeulication No. US20030105292A1

geneRAL INFORMATION:

APPLICANT: Behan, Dominic P.

APPLICANT: Liaw, Chen W.

TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION NUMBER: US/10/251,385

CURRENT APPLICATION NUMBER: US/09/170,496

PRIOR PELING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 294

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G
                                      ŋ
                                        Constitutively Activated Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 RNTAEEENSANPNODONARRRKKKERRPRGTMOAINNERKASKVLGIVFFVFLIMWCPFF 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --ERKFQANCGIDFIIFWIFWILLF 54
                                                                                                                                                                                                                                                                                                                                                                                                             269 RNTAEEENSANPNODONARRKKKKERRPRGTMOAINNERKAKKVLGIVFFVFLIMWCPFF 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                -ERKFQANCGIDFIIFWIFWILLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9; Length 458;
                                                                                                                                                                                                                                                                                                                 Length 458;
                                                                                                                                                                                                                                                                                                                                                 Indels
          APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. US20030105292A1-Endogenous, Cor
TITLE OF INVENTION: Protein-Coupled
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 67;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 RDHASLGDSETLSQTELRKKERKKKR---
                                                                                                                                                                                                                                                                                                                  Score 68;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :: |:|| |:|: |
329 ITNIL--SVLC----EKSCNQKL 345
                                                                                                                                                                                                                                                                                                                                                                                     6 RDHASLGDSETLSQTELRKKERKKKR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 SHHWIQESLLCPPSPKEVTCREML 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHHWIQESLLCPPSPKEVTCREML 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-10-225-567A-16
; Sequence 16, Application US/10225567A
; Publication No. US20030113798A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329 ITNIL--SVLC----EKSCNQKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.6%;
illarity 27.4%;
Conservative 14
                                                                                                                                                                                                                                                                                                                  th 12.8%;
Similarity 27.4%;
23; Conservative 1
                                                                                                                                                                           NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 230
LENGTH: 458
APPLICANT: Behan, Dominic APPLICANT: Chalmers, Dere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens US-10-251-385-126
                                                                                                                                                                                                                                                   ; TYPE: PRT; ORGANISM: Homo sapiens
US-10-251-385-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 23; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-10-251-385-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 126
LENGTH: 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT
                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE:
                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                              Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QΫ́
                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
GENERAL INFORMATION:
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Christine L.
APPLICANT: Roush, Christine L.
APPLICANT: APPLICANTON NUMBER: US/10/225,567A
CURRENT FILING DATE: 2000-12-19
FRIOR FILING DATE: 2000-12-19
FRI
```

		•	
			₽.

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

- protein search, using sw model OM protein 9, 2003, 15:05:28 ; Search time 43.7788 Seconds (without alignments) 213.004 Million cell update July Run on:

updates/sec

97

......LTGGCLPWATRSHLGRRKCS US-09-854-133-586 532 1 EVEVSRDHASLGDSETLSQT... Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 1 0 E 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	TP synthase Fl,	oothetical prot	scocorticoid-	scocorticold-	acocorticoi	acocorticoid-	rotonin recept	ypothetical prot	riant-specific	ypothetical prot	ct-warn	tein hom	le oxidore	probable oxidoredu	rome P450	ra	n H28G03.3	insporting	bosomal pro	ibosomal pr	able bacterio	riant-specific	pothetical pro	pothetical prot	thetical prot	matode resistan	ichohyalin – sh	ypothetical	otein B0272.5
	,																													
7.7.7.7	a	A82	3202	1047	1047	1047	1047	3061	9661	1160	1963	1020	191	9091	3576	0801	4877	8953	0607	B306	9822	8313	1402	276	2536	1952	916	4069	868	968
	DB		7	7	~	7	~	7	~	7	0	4	Н	7	7	7	7	~	7	7	7	~	7	7	7	7	7	1	7	7
		1	\sim	\sim	\sim	-4	$\overline{}$	10	85	$\overline{}$	\sim	_	$\overline{}$	C 3	C 3	_	w	O1	_	w	1	(4			ш,	.,		27	ш,	Ō
dР	Query	13.6	~	~;	~;	~;	~;	~;	~	~	ς.	~;	·~;	ζ.	ά.	ζ.	ď	α.	ij.	ä	i	H.	;	Ξ.	Ë.	$\ddot{-}$	Ή.	11.7		Ä
	Score	72	7	68	9	68	68	67	29	66.5	9	99	5	Ŋ.	65.5	Θ	64.5	Ψ	4	•	α.	4	2	d)	62	62	62	62	62	62
	Result No.	! ! . !	7	ო	4	ហ	9	7	60	თ	10		12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

1 pro F12.1 1 pro ecept prote	hypothetical prote variant surface pr pediocin PA-1 prec	cal p	rotein l prot - huma
868 557 960 332 888 NY8	7161 2843 4894	5127 2598 4857	TVMSE2 R3ZR1 T21048 W4WL11
000000	777	000	H 7 7 F
966644	2573 3026 62	787	468 568 777 108
11.7 11.7 11.7 11.6 11.6			
62 62 62 61.5 61.5	61.5 61.5 61.5	61 61 60.5	60.5 60.5 60.5
332 332 334 354	337 337 38	39 40 41	44 44 5

ALIGNMENTS

	RESULT 1 A82037 ATP synthase F1, delta subunit VC2767 [imported] - Vibrio cholerae (strain N16961 s
	C; Species: Vibrio cholerae C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
· <u></u>	C; Accession: A8203/ R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, l chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Selles l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
	Nature 405, 477-483, 2000 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301
	A;Cross-references: GB:AE004342; GB:AE003852; NID:99657358; PIDN:AAF95906.1; GSFDB: A;Experimental source: serogroup O1; strain N16961; biotype El Tor C;Genetics:
	A;Gene: VC2767 A;Map position: 1 C;Superfamily: H+-transporting ATP synthase delta chain
	Query Match 13.6%; Score 72.5; DB 2; Length 177; Best Local Similarity 32.6%; Pred. No. 0.79; Matches 15; Conservative 11; Mismatches 13; Indels 7; Gaps 1;
	Qy 4 VSRDHASLGDSETLSQTELRKKERKKKRERKFQANCGID 42 : ::
	DD 99 LKQEHEKKVDVEVISATELSEQQRSEIGSKLEQRLERKVQLNCSVD 144
	l - Caenorhabditis elegans Legans
	C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change zy-Oct-1999 C;Accession: T32024
	D. BL Data Library, July 1997
	A; Description: The sequence of C. elegans cosmid T06D4. A; Reference number: Z21113
141	A; Accession: T32024 A; Status: preliminary; translated from GB/EMBL/DDBJ
	> BL:AF016673; PIDN:AAB66123
	A; Experimental source: strain Bristol N2; clone T06D4 C; Genetics:
	SP:T06D tion: 2
_	11/ 130/31 103/41 24/31 10/16/16/16/16/16/16/16/16/16/16/16/16/16/

88 RSHLGRR 94 : 388 KSH-GRR 393 5 orticoid-induced recepto	14-Feb-1992 #sequence_rev sion: D40470 sion: D40470 gan, M.T.; Campbell, N.F.; docrinol. 5, 1331-1338, 19 : Identification of a gene ence number: A40470; MUID: Sion: D40470 s: preliminary ule type: mRNA ues: 1-443 <har> -references: GB:M80160 family: neurokinin 1 recep Match Match Local Similarity 22.8%; es 29; Conservative 1.</har>	OY 10 SLGDSETLSQTELRKKERKRERR ::	stocooperate of the cooperate of the coo	10 SLGDSETLSQTELRKKERK ::
<pre>Query Match Best Local Similarity 31.8%; Pred. No. 5.8; Matches 14; Conservative 9; Mismatches 9; Indels 12; Gaps 1; Qy 23 RKKERKKRERKFQANCGIDFIIFWIFWILLF 54 :: :: : Db 8 KEKEKERKKAEKFSADEKTANIKDRIINCVYPVILIILFWLLLF 51</pre>	RESULT 3 A40470 glucocorticoid-induced receptor precursor, short form RP39 - mouse C; Species: Mus musculus (house mouse) C; Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Apr-2000 C; Accession: A40470 R; Harrigan, M.T.; Campbell, N.F.; Bourgeois, S. Mol. Endocrinol. 5, 1331-1338, 1991 A; Title: Identification of a gene induced by glucocorticoids in murine T-cells: a pA; Reference number: A40470; WUID: 92123228; PMID: 1663214 A; Accession: A40470 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-381 < HARR> A; Cross-references: GB:M80610 C; Superfamily: neurokinin 1 receptor	Query Match Best Local Similarity 22.8%; Pred. No. 5.6; Matches 29; Conservative 11; Mismatches 41; Indels 46; Gaps 5; Qy 10 SLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWIFWILL	cursor, short form RP23 - mouse lon 14-Feb-1992 #text_change 20-Apr-2000 surgeois, S. duced by glucocorticoids in murine T-cells: a 23228; PMID:1663214	12.8%; Score 68; DB 2; Length 423; ty 22.8%; Pred. No. 6.2; servative 11; Mismatches 41; Indels 46; Gaps 5; LSQTELRKKERKKRERKFQANCGIDFIIFWIFWILL

```
luced by glucocorticoids in murine T-cells: a p.
23228; PMID:1663214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ıced by glucocorticoids in murine T-cells: a pc
8228; PMID:1663214
                                                                                                                                                                                                                                               ω
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                                                                       | : | : | ...|
VKMLVLVVVLFALCWFPLNCYVLLLSSKAIHTNNALY 347
                                                                                                                                                                                                                                                                                                                                            53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------PPSPKEVTCREMLTGGCLPWAT 87
                         n 14-Feb-1992 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n 14-Feb-1992 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | : | : | : |
|KMLVLVVVLFALCWFPLNCYVLLLSSKAIHTNNALY
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KFQANCGIDFIIFWI - - - FWILL - - - - - - - -
                                                                                                                                                                                                                                            46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46;
                                                                                                                                                                                                             re 68; DB 2; Length 443;
d. No. 6.4;
Mismatches 41; Indels
                                                                                                                                                                                                                                                                      RKFQANCGIDFIIFWI---FWILL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Te 68; DB 2; Length 491; No. 7.1; Ismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
form RP105 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    form RP82 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
                                                       rgeois, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             geois, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        456 KSH-GRR 461
```

586.rpr

-09-854-133-

ns

3

```
variant-specific surface protein 1 homolog PFB1055c - malaria parasite (Plasmodium variant-specific surface protein 1 homolog PFB1055c - malaria parasite (Plasmodium N; Alternate names: erythrocyte membrane binding protein 1 (EMP1)
C; Species: Plasmodium falciparum
C; Species: Plasmodium falciparum
C; Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C; Accession: B71600
R; Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, .; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Science 282, 1126-1132, 1998
A; Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A; Reference number: A71600; MUID:99021743; PMID:9804551
                                                                                                                                                                                                                                                               A; Reference number: A71600; MUID: 99021743; PMID: 9804551
A; Accession: B71600
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-2197 <GAR>
A; Residues: 1-2197 <GAR>
A; Cross-references: GB: AE001434; GB: AE001362; NID: g3845341; PIDN: AAC71996.1; PID: g3
A; Experimental source: clone 3D7
C; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein B5022.170 [imported] - Neurospora crassa C; Species: Neurospora crassa C; Species: Neurospora crassa C; Species: Neurospora crassa C; Species: O2-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000 C; Accession: T49635 R; Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyaki Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyaki Submitted to the Protein Sequence Database, May 2000 A; Reference number: 225022 A; Reference number: 225022 A; Reference number: 225022 A; Schulte, DNA A; Residues: preliminary A; Molecule type: DNA A; Residues: 1-13 cscH> A; Residues: 1-13 cscH> A; Reserimental source: BAC clone B5022; strain OR74A C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Map position: 6 C; Superfamily: Neurospora crassa hypothetical protein B5022.170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F40201
artifact-warning sequence (translated ALU class F) - human
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C;Accession: F40201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --FILEWI--FWILLESHHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSVTTTRIWGRKEKKKKKRRKKRTEQGNAKDGDTTVNADGQRSVVGWLVGFWPSLHHHAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 602 EVOKVKDDKN-GEEEDEDEDVDKVKKAGGLCILENKKHESRNNSSNEPEQFOKTFHDFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      დ
ც
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      661 YFWIGRFLNDSMYWRGKVNSCINNPKRKKCRNECKDDC--GCFKEWIGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 IFWIFWILLFSHHWIQESLLCPPSPKEVTCREMLTGGCLPWATRSHLGRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --KERKKKRERKFQAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASLGDSETLSQTELRKKERKKKRERKFQANCGID-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 66; DB
Pred. No. 3.3;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ed. No. 47;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.5%; Score 66.5; 24.3%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVEVSRDHASLGDSETLSQTELRK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | : | : | | | | : | : | VHELSTITVHHQLNPPPAPLSMPC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -SILCPPSPKEVIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 25.0%;
Matches 21; Conservative 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 27; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IQE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  smitter receptor; transme
                                                                                                                                                                                                                                                                                                                                                                                           activ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1351/3; 1495/3;
                                                                                                                                                                                                                                                                                                                                                                                           which
                                                                                                                                                             S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                             M.; Felder
                                                                                                                                                                                                                                                                                                                                                             D:9338028
.o G-proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; CESP:C46C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-oct-1999
                                                                                                      13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -ERKFQANCGIDFIIFWIFWILLF
                                                                                                                                                                                                                   subtypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1096/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                               Jaye,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein C46C2.1 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15
C; Accession: T19964
R; McMurray, A.
submitted to the EMBL Data Library, December 1995
A; Reference number: Z19204
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-1851 <WIL>
A; Cross-references: EMBL: Z68296; PIDN: CAA92591.1; GSPDB: GN00022; C; Genetics:
C; Genetics:
                                                                                                                                                                                                                      receptor
                                                                                                    #text_change
                                                                                                                                                                                                                                                                                                                                                                  \mathbf{PI}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurotran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65/2; 93/3; 239/2; 340/1; 448/3; 863/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                  Residues: 1-458 <SAL>
Cross-references: GB:M81778; NID:g338027; PIDN:AAA60317.1; F
Comment: This receptor protein is membrane-bound and couple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            658
                                                             Nationale names: 3.1Moloxyllyplanine recepcus 10 (3 ninls)
C; Species: Homo sapiens (man)
C; Accession: JS0616
R; Saltzman, A.G.; Morse, B.; Whitman, M.M.; Ivanshchenko, Y.;
Biochem, Biophys. Res. Commun. 181, 1469-1478, 1991
A; Title: Cloning of the human serotonin 5-HT2 and 5-HT1C rece
A; Reference number: JS0615; MUID:92109767; PMID:1722404
A; Reference number: JS0615; MUID:92109767; PMID:1722404
A; Molecule type: mRNA
A; Residues: 1-458 <SAL>
A; Cross-references: GB:M81778; NID:9338027; PIDN:AAA60317.1;
C; Comment: This receptor protein is membrane-bound and couple
C; Genetics:
A; Gene: GDB:HTR2C; HTRIC
A; Genetics:
A; Gene: GDB:HTR2C; HTRIC
A; Genetics:
C; Genetics:
A; Genetics:
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43
                                             (5-HTR1C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEVSRDHASLGDSETLSQTELRKKERKKKRERKFQANCGIDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                      in receptor 1C - human
late names: 5-hydroxytryptamine receptor 1C
is: Homo sapiens (man)
31-Mar-1992 #sequence_revision 31-Mar-1992
ion: JS0616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 67; DB 2
Pred. No. 8.7;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 67; DB;
Pred. No. 35;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 RDHASLGDSETLSQTELRKKERKKRP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---EKSCNOKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHHWIQESLLCPPSPKEVTCREML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.6%;
illarity 33.3%;
Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.6%;
larity 27.4%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITNIE--SVEC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity
23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e: CESP:C46C2.1
position: 4
rons: 15/3; 42/1
                                                    N; Alternate names
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: CES
A;Map posit
A;Introns:
                          serotonin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
```

-CGIDEI 44

Gaps

Э.

```
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-207 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB35720.1; PID:g13361763; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs2297
C;Superfamily: Escherichia coli ycdY protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-514 <TIJ>>
A;Cross-references: EMBL:AF030260; NID:g4204094; PIDN:AAD10204.1; PID:g4204095 C;Genetics:
A;Gene: vagh111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytochrome P450 CYP94Al - spring vetch
C;Species: Vicia sativa (spring vetch, tare)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change
C;Accession: T08014
R;Tijet, N.; Helvig, C.; Pinot, F.; le Bouquin, R.; Lesot, A.; E
Biochem. J. 332, 583-589, 1998
A;Title: Functional expression in yeast and characterization of
A;Reference number: 216287; MUID:98264856; PMID:9601090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
A;Residues: 1-514 <TIJ>
                                                                                                                                                                                                                                         Similarity 25; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
25; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T08014
                                                                                                                                                                                                                 Query Match
Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
F85764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
T08014
                                                                                                                                                                                                                                                                                                                                            Д
                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                      δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                               pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ပ္ပ
                                                                                                                                                                                           other potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        years protein homolog b1591 - Escherichia coli (strain K-12)
C; Species: Escherichia coli
C; Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
C; Accession: A64915
R; Blattner, F. R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MuID: 97426617; PMID: 9278503
A; Reference number: A64720; MuID: 97426617; PMID: 9278503
A; Reference number: A64915
A; Ratus: nucleic acid sequence not shown; translation not shown
A; Residues: 1-207 < BLAT>
A; Residues: 1-207 < BLAT>
A; Residues: 1-207 < BLAT>
A; Cross-references: GB: AE000254; GB: U00096; NID: 91787862; PIDN: AAC74663.1; PID: 91787874; C; Superfamily: Escherichia coli ycdy protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gend
                                                                                                                                                                                                                                                          of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0157:H7
                                                                                                                                                                                                                                                                                                  a portion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ö
                                                                                                                                                                                                                                                         reading frames
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a coli 0157:H7 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yokoyama, K.; Han,
shinagawa, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ia coli (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWIFWILLFSHHWIQESLLCPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLFSHHWIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shinagawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                 ಭ
                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                  anence
                                                                                                                                                                                                                                                         ဖ
                                                                                                                                                                                           ived
R; Claverie, J.M.

personal communication, 1992
A; Reference number: A40201
A; Accession: F40201
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-673 <CLA>
R; Claverie, J.M.
Genomics 12, 838-841, 1992
A; Title: Identifying coding exons by similarity search: Alu-derived
A; Reference number: A40200; MUID:92241891; PMID:1572661
A; Contents: annotation
C; Comment: This "warning" entry is a conceptual translation in all in-frame stop codons are shown as 'x'.
C; Comment: Any significant similarity of a predicted protein sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                         all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Escherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 0
C; Accession: A90916
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; S DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichi A; Reference number: A99629; MUID: 21156231; PMID: 11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEVSRDHASLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWIFWI
                                                                                                                                                                                                                                                                                                                                                           Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherich
                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                  31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable oxidoreductase component ECs2297 [imported]
                                                                                                                                                                                                                                                                                                                                                       ore 66; DB 4;
ed. No. 17;
Mismatches 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 65.5; Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --NGROTECEELLAWHLFPWSTR 164
                                                                                                                                                                                                                                                                                                                                                       Score 66;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLLCPPSPKEVTCREMLTGGCLPWATR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 PKEVICREMLIGGCLPWATRSHLGRRKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --QWOVLAH--
                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                  12.4%;
ilarity 21.3%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.3%;
.Similarity 28.7%;
25; Conservative 1
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 PAGV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
A90916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A64915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
probable oxidoreductase component Z2581 [imported] - Escherichia coli (strain 0157: C; Species: Escherichia coli C; Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C; Accession: F85764

R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; M iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apo Nature 409, 529-533, 2001

A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A; Reference number: A85480; MUID:21074935; PMID:11206551

A; Coss: references: GB:AE005174; NID:912515566; PIDN:AAG56578.1; GSPDB:GN00145; UWG. A; Experimental source: strain O157:H7, substrain EDL933

C; Genetics: A; Gene: Z2581

C; Superfamily: Escherichia coli ycdy protein
                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                      143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143
                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                               2 VEVSRDHASLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWIFWILLFSHHWIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEVSRDHASLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWILLFSHHWIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VWLDRESXLFGDS-TLA---LRQWMREKGIQFEMKQNEPEDH----FGSLLLMAAWLAE
                                                                 Gaps
                                                             15;
        Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 207;
                                                               Indels
                                                          33;
   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
        DB
 Score 65.5; D
Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.3%; Score 65.5; DE 28.7%; Pred. No. 5.9;
                              ed. No. 5.9 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ed. No. 5.9 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : :: | |:| ||:||
--NGRQTECEELLAWHLFPWSTR 164
                                                                                                                                                                                                                                   SLLCPPSPKEVTCREMLTGGCLPWATR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli ycdy protein
                                                                                                                                                                                                                                                                         : :: | |:| | |:| --NGRQTECEELLAWHLFPWSTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 SLLCPPSPKEVTCREMLTGGCLPWATR
                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
12.3%;
larity 28.7%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
```

a clofibrate-inducit

Salaun,

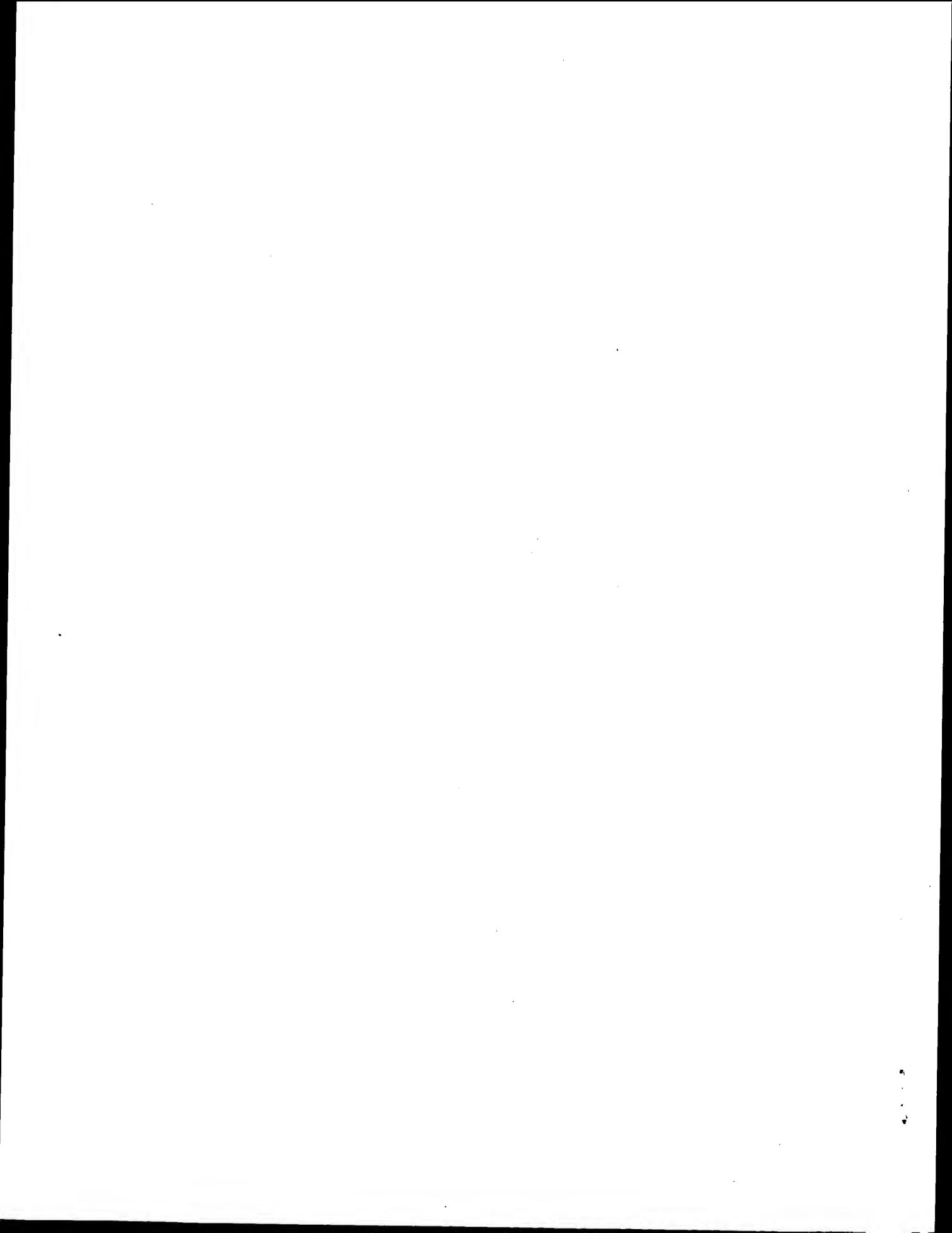
F. ;

A.; Durst,

21-May-1999 #text_change 16-Feb-2001

	Db 366 ALSESMRLYPPVPMDSKEAVNDDVLPDGWVVRNGIIVIIHVIAMGRAAN 413
--	--

Search completed: July 9, 2003, 15:09:4 Job time: 46.7788 secs



```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

9, 2003, 15:05:28 ; Search time 12.0177 Seconds (without alignments) 334.773 Million cell updates/sec July Run on:

US-09-854-133-586 532 1 EVEVSRDHASLGDSETLSQT......LTGGCLPWATRSHLGRRKCS Title: Perfect score: Sequence:

Gapext 0.5 BLOSUM62 Gapop 10.0 Scoring table:

112892 seqs, 41476328 residues Searched:

112892

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	escription	0731 mus muscul	8335 homo s	6174 escheri	81117 vicia	50 xenopus la	37	r3 pseu	93	72 clos	59 homc	29 rhizok	hum	30 pedi	37 mus mu	16 human	eg hum	89	22 sac	20	71	0407 cavi	2304 mus mu	2305 rattus	5367 homo sa	9578 gallus	45481 mus mus	9279	47148 sacch	08909 rattus no	5745	7321 rattus n	7665 drosophi	02787 homo sapien
SUMMARIES	QI QI	GP72_MOUS	5H2C_HUMAN P	I_ECOLI	1_VICSA	XENLA	_VIBAL	_PSEAE	SHEEP	1_CLOPE	_HUMAN	RHIME	_HRV89	_PEDAC	2_MOUSE	HPV11	HPV6C	MOUSE	_YEAST	Сніск	2_HUMAN	_CAVPO	MOUSE	RAT	_HUMAN	з_сніск	_MOUSE	HUMAN	81_YEAST	_RAT	L4_BRARE	CAL_RAT	RY	TRFE_HUMAN P
	DB	П	Н		7		Н	Н	, †	-	,	Н	-	Н	Н		, 	Н	Н		Н	~	~ −1	~	, - 1	П	7	7	7	П	٦	1	~	Н
	Length	423	458	0		S	~	72	4	7	~	9	9	9	9	0	0	\mathbf{c}	œ	\sim	333	4	4	4	8	63	4	44	œ	9	7	S	351	σ
di	Query Match	2.8	12.6	ų.	ά.	ä	;	.	;		;	· 	;	;	, ,	1	H	<u>.</u>	H	٦.	.	H	;	.		i	H.	;	1.	;	Ţ.	Η.	.	.
			9			9		ς.	9		:	:	:	9					9	ю О	59.5	σ.	თ	о О	6	<u>.</u>	о О	9				Ω.	58.5	ф Ф
	ì	1	7	m	4	ហ	9	7	ထ	Q	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P56566 mus musculu	P53724 saccharomyc	014966 homo sapien	macac	P40986 saccharomyc	P11267 simian immu	P91620 drosophila	P91621 drosophila	Q9wv06 mus musculu	P38487 bacillus sp	Q8vc56 mus musculu	P38361 saccharomyc
S103_MOUSE	YN8C_YEAST	RB7L_HUMAN	B2AR_MACMU	CC1_YEAST	ENV_SIVML	SIF2_DROME	SIF1_DROME	ANR2_MOUSE	CREA_BACSP	RNF8_MOUSE	YB81_YEAST
1	Н	۲	1	m	Н	Н	1		Н	-4	Н
101	139	203	415	491	880	2044	2064	328	410	488	574
10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.8	10.8	10.8	10.8
58	58	58	58	58	58	28	58	~		57.5	

ALIGNMENTS

423 AA.	update) on update)		data: Vertebrata: Enteleostomi:	**			a gene induced by glucocorticoids in murine al G protein-coupled receptor.";	domonata v antimonatoria v ad dii	protein.	FORMS OF GIR MAY ARISE BY	THYMUS AND SPLEEN.	AND CAME; IN I CELLS. 1 OF G-PROTEIN COUPLED RECEPTORS.		ht. It is produced through a collaboration	te. There are no restrict	as its content is	veu. Usaye by See http://www.i	b.ch).							nembrane; Glycoprotein; Signal;		PROBABLE G PROTEIN-COUPLED RECEPTOR	EXTRACELLULAR (POTENTIAL).	1 (POTENTIAL). CYTOPLASMIC (POTENTIAL).	Ġ	EXTRACELLULAR (POTENTIAL).	OTENTIAL).
PRT;	Created) Last sequence up Last annotation	ed receptor		Rodentia; Sciu		PubMed=1663214; pbell N.F., Bour	e induced rotein-cou	1338(1991)	riok. Integ	: MULTIPLE	SRAIN,	ORITCOI FO FAMI	; ; ; ; ; ;	ry is copyright.	Inst	Ħ		license@isb-sib.ch)	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		GPCR_Rhodpsn.	DOPSN.	PROTEIN_RECEP_F1_1;	- 1		POTENTIAL	PROBA	EXTRA	CYTOP	2 (PO	EXTRA	
STANDARD;	25, 32, 40,	n-cor				8; PubMed	of a geno	5:1331-	LOCATION:	ጁ ወ	, <u>H</u> .	ELONGS	!	ent	J.		ıs statement es a license	1 to lice	AA17882.1:	Gir.	0276; GPCR_Rhod	GPCRRHO	7; G_PROT	2; G_PROT	ed receptor;	17	423			129		
SE	1993 (Rel 1995 (Rel 2001 (Rel	ு வீ ந	sculus (Mouse ota: Metazoa:	ia; Eutheri	FROM N.)212322 M.T.,	tion pote	Endocrinol	SUBCELLULAR	SRNATIVE SRNATIVE	TISSUE SPECIF	LARITY:		- PF	European Bioin	non-pr	and ch requir	an emai	30481: A	1:95712;); IPROO	PR00237	PS0023	PS5026	ive spl	NAL 1 1	18	₩ (~ 6		13	
LT I _MOUSE GP72_MOUS	H C B -	Probable induced	Mus musc	Mammalia; F NCBI_TaxID=	[1] SEQUENCE	MEDLINE=921 Harrigan M	"Identif	Mol. Enc	1	-!- ALTE		l I		This SWI	the Euro	use by	entities	ы	EMBL: MS	MGD; MG]	InterPro	PRINTS:	PROSITE;	PROSITE	G-prote	SIGNAL	CHAIN	DOMAIN	TRANSMEM	TRANSMEM	DOMAIN	THE PARTY OF THE P
72	A L L L L	D E				RX RA	RT	R.	38	ပ္ပင္ပ	ខ្លួ	38	ည	ပ္ပ ပ	3 8	ပ္ပ (3 8	ဦ	CC DR	DR	DR	DR.	DR	DR	X X	FT	FT	→ E+ E 4 E+ I	- E-	FT	FT	******

```
5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                387
                                                                                                                                                                                                                                                                                                                                                                                                                           53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87
                                                                                                                                                                                                                                 DGGELRSPSVTF
PPLE (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -PPSPKEVTCREMLTGGCLPWAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVPSFRVAWTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKAIHTNNALY
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding
                                                                                                                                                                                                                                                                                    N ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subtypes
                                                                                                                                           (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Τ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    re M.,
                                                                                                                                                                                                                                                                                                                                                                                       46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             er
4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIN-
N-LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J., De Bc
                                                                                                                                                                                                                                                                                                                                                                                                                                              FAFHWFAMSSTCYNPFIYCWINENFRVELKALLSMCORPPKPQEDRLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recep
                                                                                                                                                                                                                                                                                                                                                      Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 serotonin 5-HT2 and 5-HT1C receptor . Commun. 181:1469-1478(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                          --FWILL
                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                 ORPWDFQESOSLHDTLFPPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Brain;
MEDLINE=92109767; PubMed=1722404;
Saltzman A.G., Morse B., Whitman M.M., Ivanshchenko Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | [2]
| SEQUENCE FROM N.A., AND FUNCITOR.
| SEQUENCE FROM N.A., AND FUNCITOR.
| TISSUE=Placenta, and Hippocampus;
| MEDLINE=95203331; PubMed=7895773;
| Stam N.J., Vanderheyden P., Van Alebeek C., Klomp J.,
| Van Delft A.M.L., Olijve W.;
| "Genomic organisation and functional expression of the the human serotonin 5-HT2C receptor.";
| the human serotonin 5-HT2C receptor.";
| Eur. J. Pharmacol. 269:339-348(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN STANDARD,
5H2C_HUMAN STANDARD,
P28335; Q9NP28;
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chang L.-S
                                                                                                                                                                                                                                                                                                                                                                                                                       SLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWI-
                                                                                                                                                                                                                                                                                                                                                                                       41;
                                                                                                                                                                                                                                                                                                                  3ACE43452BF15391
                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                     3.8;
                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Brain;
MEDLINE=97001158; PubMed=8812491;
Xie E., Zhao L., Levine A.J., Shenk T.,
                                                                                                                                                                                                                                                                                                                                                    Score 68;
                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                   RP10
                                                                                                                                                                                                                                                                                                                                                                    Pred
                                                                                                                                                                                                                                                                                  Ø
                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                   12.8%;
larity 22.8%;
Conservative
                                                                                                                                                                                                                                                                                                                    48136
  208
2238
2238
3315
3315
348
348
348
171
171
                                                                                                                                                                                                                                                                               171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSHHWIQESLLC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|| |||
KSH-GRR 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5-hydroxytryptamine
(5HT-1C).
HTR2C OR HTR1C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94
                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                   Similarity 29; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSHLGRR
  187
239
239
239
239
332
332
34
34
1130
1130
                                                                                                                                                                                                                                                                                171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                    423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
                                                      DOMAIN
TRANSMEM
                                                                                                       TRANSMEM
DOMAIN
                                                                                                                                        CARBOHYD
CARBOHYD
                                                                                                                                                                         CARBOHYD
DISULFID
VARSPLIC
VARSPLIC
    TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Felder S. "Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                      10
                                                                                                                                                                                                                                                                                                                                                                                                                                                       271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328
                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              388
                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem.
                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H2C_I
                                                     Q
D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 049310; AAB40898.1; -.

REMBL; AC004822; AAC71658.1; -.

REMBL; AC004822; AC0276; GPCR_Rhodpsn.

REMBL; AC0001; 7tm_1; 1.

REMBL; AC0001; 7tm_1; 1.

REMBL; AC0001; 7tm_1; 1.

REMSTE; PSO0237; G_PROTEIN_RECEP_F1_1; 1.

REMSTE; PSO0237; G_PROTEIN_RECEP_F1_2; 1.

REMSTE; PSO0237; G_PROTEIN_RECEP_F1_2; 1.

REALSTE; PSO0237; G_PROTEIN_RECEP_F1_2; 1.

REALSTER SOURT FARACELULAR (POTENTIAL).

TRANSMEM 53 78 (POTENTIAL).

TRANSMEM 128 150 3 (POTENTIAL).

TRANSMEM 121 193 4 (POTENTIAL).

TRANSMEM 171 193 4 (POTENTIAL).

TRANSMEM 171 193 4 (POTENTIAL).

TRANSMEM 171 193 4 (POTENTIAL).

TRANSMEM 214 213 5 (POTENTIAL).

TRANSMEM 214 235 5 (POTENTIAL).
                                                                                                                                                                                                                                                events within the
                       genomic
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-116 FROM N.A.
Kalicki J., Mead K.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                     CDNA,
                                                                                                                                                                                                                  R.B.;
RNA editing
complete c
                 "The human serotonin 5-HT2C receptor: completestructure, and alternatively spliced variant. Genomics 35:551-561(1996).
                                                                                                                            SEQUENCE FROM N.A., AND RNA EDITING.
TISSUE=Brain;
MEDLINE=99127198; PubMed=9928237;
Niswender C.M., Sanders-Bush E., Emeson
"Identification and characterization of
5-HT2C receptor.";
Ann. N.Y. Acad. Sci. 861:38-48(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M81778; AAA60317.1
EMBL; X80763; CAB59978.1
EMBL; U49516; AAB40898.1
                                                                                                                                                                                                                                                                 5-HT2C
Ann. N.
                                                                                                                                                                                                                                                                                                                              5]
                                                                                                                                                                                                                                                                                                                                                                                                                                        [9]
                                                                                                                              THE TEXT STANDAR STAND
```

3

```
FIIFWIFWILLE
                                                                                                                                                                                                                                                                                                                                      269 RNTAEEENSANPNODONARRKKKERRPRGTMQAINNERKASKVLGIVFFVFLIMWCPFF
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burland V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D.J
                                                            NTIAL)
                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      К.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D
                                                                                                                                                                                 I -> V (IN RNA EDITED VERSION).
/FTId=VAR_010168.
9E76B3FFD3E09C93 CRC64;
                                                                                                    /FTId=VAR_003450.

I -> V (IN RNA EDITED VERSION).
/FTId=VAR_010166.

N -> S (IN RNA EDITED VERSION).
/FTId=VAR_010167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage many Res. 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97251357; PubMed=9097039;
Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mo Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
                                                                                                                                                                                                                                                                                                          --ERKFQANCGID
                                                                                                                                                                                                                                               Length 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12."
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                             Indels
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YNFI_ECOLI STANDARD; PRT; 207 AA. P76174; P77270; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 16-JUL-1998 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical protein ynfI precursor. YNFI OR B1591 OR 22581 OR ECS2297. Escherichia coli, and Escherichia coli 0157:H7.
                                                        N-LINKED (GLCNAC.
BY SIMILARITY.
                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                               Pred. No. 5.4; ; Mismatches
                                                                                                                                                                                                                                                 Score 67;
                                                                                                                                                                                                                                                                                                            RDHASLGDSETLSQTELRKKERKKR--
                                                                                                                                                                                                                                                                                                                                                                      SHHWIQESLLCPPSPKEVTCREML 78
                                                                                                                                                                                                                                                                                                                                                                                                    --EKSCNOKL
                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                    51821 MW;
                                                                                                                                                                                                                                                 12.6%; 27.4%;
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamamoto Y., Horiuchi T
"A 570-kb DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                      329 ITNIL--SVLC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=562, 83334;
333
348
371
458
207
23
                                                                                                                                                                                   160
                                                                                                                          156
                                                                                                                                                       158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                Similarity 23; Conser
                                                                                                                                                                                                                    458 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Riler
Gregor J., Dav...
Shao Y.;
                                                                                                                                                                                    160
312
334
349
373
39
127
23
                                                                                                                          156
                                                                                                                                                       158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Motomus.
Oshima T., Sar
Tagami H., Tal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=K12;
                                                                                                                                                                                                                                                                                                              9
                DOMAIN
TRANSMEM
DOMAIN
                                                                             DISULFID
VARIANT
                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                 Query Match
   TRANSMEM
                                                                CARBOHYD
                                                                                                                                                                                                                                                                  Local
                                                                                                                          VARIANT
                                                                                                                                                         VARIANT
                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YNFI_ECOLI
                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                    Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RN
RP
RC
RX
RX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RA
RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RA
RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RA
RA
RA
RA
                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                            δŏ
                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                        FT
                                                                                                                                                                                                                                                                                                                ŏ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vicia sativa (Spring vetch) (Tare).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Vicia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEVSRDHASLGDSETLSQTELRKKERKKKRERKFQANCGIDF11FW1FW1LLFSHHW1QE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VWLDRESVLFGDS-TLA----LRQWMREKGIQFEMKQNEPEDH-----FGSLLLMAAWLAE
                                                                                                                                                                               ×.
                                                                                                                                                                                K., Ishii K., Yokoyama
J., Tanaka M., Tobe T.,
                                                                                                                                             STRAIN=0157:H7 / RIMD 0509952;
STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama Hayashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
-! SIMILARITY: TO H.INFLUENZAE HI1044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Œı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
              - ⊻
                                                                        O157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Durst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last annotation update)
(EC 1.14.-.-) (P450-dependent fatty acid
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L. Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Seedling;
MEDLINE=98264856; PubMed=9601090;
Tijet N., Helvig C., Pinot F., Le Bouquin R., Lesot A.,
Salauen J.-P., Benveniste I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL PROTEIN YNFI 458DDBF76D16EA89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     514 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Cytochrome P450 94A1 (EC 1.14.-.-) (P450-de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 65.5; D) Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d. No. 3.4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLLCPPSPKEVTCREMLTGGCLPWATR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --NGROTECEELLAWHLFPWSTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE000254; AAC74663.1; -.
D90801; BAA15315.1; ALT_INIT.
D90802; BAA15325.1; ALT_INIT.
AE005382; AAG56578.1; -.
AP002557; BAB35720.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.3%; ; illarity 28.7%; l Conservative 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23646 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                             "Genome sequence of ente
Nature 409:529-533(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LUGGene; EG13847; ynfl
Hypothetical protein; S
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          omega-hydroxylase).
CYP94A1 OR VAGH111.
Vicia sativa (Sprin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34
207 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
25; Conser
                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C941_VICSA
O81117;
15-JUN-2002
15-JUN-2002
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC
DT
DT
DT
DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             фQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                        Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                     RA
RA
```

.;

61

```
a collaboration
                                                                                                                                                                                                                                                                                  and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365
                                                                                                                                                                                                                                       EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57
                                                                      fatty acids
                                                                                                                                                                                                                                                    restrictions on
                          in monomers
                                                                                                                                                                                                                                                                          ou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVKEMVYTHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -RKFO
          clofibrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -LFSHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSGHSDEDFV
                                                                                                                                             reticulum (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  related
                                                                                                                                                                                                                                                                         in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sociated
                                                                      various fatty specificity is
                                                                                                                   cutin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95
                                                                                                                                                                                                                                                                       is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor
"Functional expression in yeast and characterization of a inducible plant cytochrome P-450 (CYP94A1) involved in cut; synthesis."; Biochem. J. 332:583-589(1998).

-!- FUNCTION: Catalyzes the omega-hydroxylation of various (FA) from 10 to 18 carbon atoms. The substrate specific higher for laurate > palmitate > myristate > linolenate linoleate > oleate > caprate. May play a minor role in synthesis and could be involved in plant defense.
                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by ancentities requires a license agreement (See http://www.isb-sor.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97109511; PubMed=8951791;
Devic E., Paquereau L., Vernier P., Knibiehler B., Audigier "Expression of a new G protein-coupled receptor X-msr is ass with an endothelial lineage in Xenopus laevis.";
Mech. Dev. 59:129-140(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 ADIVISFILAGKDTTSAALTWFFWLLWKNPRVEEEIVNELSKKSELMVYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALSESMRLYPPVPMD--SKEAVNDDVLPDGWVVKKGTIVTYHVYAMGRMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --HLGRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo:
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipida:
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 514;
                                                                                                                                                       SIMILARITY:

SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ME (BY SIMILARITY).
3D9361380D6C3B0E CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P79960; P70058;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
G Protein-coupled receptor APJ homolog (Angiotensin protein) (Mesenchyme-associated serpentine receptor)
X-MSR OR XAngiol.
                                                                                                                                                                                                                                                                                                                                 EMBL; AF030260; AAD10204.1; -.
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; FALSE_NEG.
Oxidoreductase; Monooxygenase; Heme; Transmembrane; Endoplasmic reticulum; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WIQESL-LCPPSPKEVTCREMLTGGCLP--WATRS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 RDHASLGDSETLSQ--TELR----KKERKKKRE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.2%; Score 65; 20.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -IEWIEWIL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59110 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                              29
                                                                                                                                        SUBCELL
similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANCGIDFI - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            514 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APJ_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
APJ_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best
                             Q
D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                            TISSUE SPECIFICITY: At the gastrula stage, exclusively expressed in the mesodermal layer and at the neurula stage in the lateral plate mesoderm. Larval expression is observed in the endothelium of the primary blood vessels and the forming heart.

DEVELOPMENTAL STAGE: First expressed at the late blastula stage, increases during gastrulation and remains constant between neurula
                                                                 FUNCTION: Putative receptor for an apelin-like peptide coupled to G proteins that inhibit adenylate cyclase activity.

SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                     OF G-PROTEIN COUPLED RECEPTORS.
                              expressed in vascular precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
P -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWIFWILLFSHHWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Transmembrane.
EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
                                                     Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> S (IN REF. 2)
1BF757D865057621
                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPKUUUL,,,
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ATP synthase delta chain (EC 3.6.3.14).
ATPH OR UNCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 (POTENTIAL)
CYTOPLASMIC (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ed. No. 11;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 63;
                                                                                                                                                                                                   and larva stages.
SIMILARITY: BELONGS TO FAMILY 1
          Saha M.S., Oakes J.A., Miles R.R.;
"XAngiol, a novel Xenopus gene, is
                                                                                                                                                                                                                                                                                                                                                            EMBL; X93045; CAA63612.1; -.
EMBL; U72029; AAB17004.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
72
95
109
131
150
173
150
229
229
248
270
270
270
270
270
19
353
40303 MW;
1-303 FROM N.A. Oakes J.A., Mile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.8%;
30.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L Similarity
15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39
62
73
110
132
151
174
207
2295
318
119
150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATPD_VIBAL
P12987;
01-JAN-1990
                                         cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
ATPD_VI
                                                                 DT DT DT OC OC OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID
```

ö

Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.

Wed

```
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   тнн.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRHY_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FI
FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80000
                                                                                                            THE WAY BURNERS REPRESENTED TO SOUTH THE WAY BURNERS OF SOUTH THE WAY B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN=ATCC 15692 / PAO1;

STRAIN=ATCC 15692 / PAO1;

STRAIN=ATCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-O.T., Fulfinagle W.O., Kowalik D.J., Lagrou M., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Brody L.L., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. (CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C. SIMILARITY: BELONGS TO THE ATPASE DELTA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no restrictions on ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC
                                                                                                            MEDLINE=90016889; PubMed=2529481;
Krumholz L.R., Esser U., Simoni R.D.;
Krumholz L.R., Esser U., Simoni R.D.;
"Nucleotide sequence of the unc operon of Vibrio alginolyticus.";
Nucleic Acids Res. 17:7993-7994(1989).
-!- FUNCTION: THIS PROTEIN SEEMS TO BE PART OF THE STALK THAT LINKS
CF(0) TO CF(1). IT EITHER TRANSMITS CONFORMATIONAL CHANGES FROM
CF(0) INTO CF(1) OR IS IMPLICATED IN PROTON CONDUCTION.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nd for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                  THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPHY_PSEAE STANDARD; PRT; 728 AA.

Q9HWR3;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable bacteriophytochrome (EC 2.7.3.-) (Phytochrome-li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isb.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; ATP synthesis; CF(1); Hydrogen ion transport. SEQUENCE 177 AA; 19489 MW; E8A311993DA63E4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : ::| | | : | | | : | | | : | | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- RKKKRERKFQANCGID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                    CF(1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPONENTS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 62.5; Di
Pred. No. 6.2;
.0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00125; ATPASEDELTA.
TIGRFAMS; TIGR01145; ATP_Synt_delta; 1.
PROSITE; PS00389; ATPASE_DELTA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 VSRDHASLGDSETLSQTELRKKE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P00831; 1ABV.
InterPro; IPR000711; ATPSYNT_OSCP.
Pfam; PF00213; OSCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    P: F-TYPE ATPASES HAVE AND CF(0) - THE MEMBRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X16050; CAA34178.1; -. 506079; S06079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.7%;
30.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 14; Conserv
                                                                  SEQUENCE FROM N.A.
                                                                                                     STRAIN=138-2;
MEDLINE=90016889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BPHP OR PA4117
NCBI_TaxID=663;
                                                                                                                                                                                                                                                                                                                                                                                                            H(+)(Ont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S06079;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BPHY_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                           1
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DR
 OX
RN
RC
RX
RX
RA
RT
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in included use by non-profit institutions as long as its content is commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                            There are no restrictions on it as its content is in Transfer its content is in the red.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -WIEWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                       SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE PHYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY)
FUNCTION: PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE R FORM THAT ABSORBS MAXIMALLY IN THE REGION OF THE SPECTRUM AND THE FR FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION (BY SIMILARITY). PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -EMLTGGCLPWA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGIDFIIF ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --FRHEEVHRIRWGGKPEKLLTIGPSGPRLTPRGSFEAWEEVVRGHSTPWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; PS50046; PHYTOCHROME_2; 1.
transduction; Transferase; Kinase; Phosphorylation
ceptor; Phytochrome; Chromophore; Complete proteome
17 495 CHROMOPHORE BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HISTIDINE KINASE.
CHROMOPHORE (POTENTIAL).
PHOSPHORYLATION (AUTO-) (
EEE9259392E5C4B0 CRC64;
                                                                                                                                                                                                                SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRHY_SHEEP STANDARD; PRT; 1549 AA. P22793; 01-AUG-1991 (Rel. 19, Created) 01-OCT-1994 (Rel. 30, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00360; phytochrome; 1.
Pfam; PF00512; signal; 1.
Pfam; PF01590; GAF; 1.
Pfam; PF01590; GAF; 1.
Pfam; PF01590; GAF; 1.
PRINTS; PR00344; BCTRLSENSOR.
PRINTS; PR01033; PHYTOCHROME.
SMART; SM00065; GAF; 1.
SMART; SM00387; HATPase_c; 1.
SMART; SM00388; HisKA; 1.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50146; PHYTOCHROME_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --QESLLCPPSPKEVTCR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.7%; Score 62.5; 1
23.4%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ed. No. 27;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDSETLSQTELRKKERKKKRERKFQAN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P02933; 1JOY.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR004358; Bact_sens_pr_C.
InterPro; IPR003018; GAF.
InterPro; IPR004359; HIS_KIN_sig.
InterPro; IPR003661; His_kinA.
InterPro; IPR001294; Phytochrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80930 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE004828; AAG07504.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 LLFSHHWI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            728 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               510
247
513
                                                                                                                                         SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Photoreceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trichohyalin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sensory
```

ι V

426

51

dsr.

586

ı

-133

-09 - 854

ns

```
is in no way
d for commercial
sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: HOMODIMER (PROBABLE).
-!- ALTERNATIVE PRODUCTS: AT LEAST TWO FORMS MAY BE PRODUCED BY
ALTERNATIVE SPLICING OF THE SAME GENE.
-!- TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES SUCH AS
THE INNER ROOT SHEATH (IRS) OF HAIR FOLLICLES AND MEDULLA, AND IN
THE EPITHELIA OF THE TONGUE, HOOF AND RUMEN.
-!- DOMAIN: CONSISTS OF NINE DOMAINS. DOMAIN 1 CONTAINS TWO EF-HAND
CALCIUM-BINDING DOMAINS. DOMAINS 2-4, 6, AND 8 ARE ALMOST
ENTIRELY ALPHA-HELICAL, CONFIGURED AS A SERIES OF PEPTIDE REPEATS
OF VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINGLE-STRANDED
ALPHA-HELICAL ROD STABILIZED BY IONIC INTERACTIONS.
THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS
THE MOLECULE. DOMAIN 9 CONTAINS THE C-TERMINUS, CONSERVED AMONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            outstation
                                                                                                                                                                                                                                                               FUNCTION: INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRANULAR LAYER OF THE EPIDERMIS. IT LATER BECOMES CROSS-LINKED TO KIF BY ISODIPEPTIDE BONDS. IT MAY SERVE AS SCAFFOLD PROTEIN, TOGETHER WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN ITS OWN CALCIUM-DEPENDENT POSTSYNTHETIC PROCESSING DURING TERMINAL DIFFERENTIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUES SUCH AS
LLA, AND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gh a collabora
EMBL outstati
strictions on
t is in no
                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARE
DEIMIDASE.
S-100
                                                                                                                                                                       follicles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (LOW AFFINITY) (POTENTIAL).
2 (HIGH AFFINITY) (POTENTIAL)
AA APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EME the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content impositied and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sior send an email to license@isb-sib.ch).
              SEQUENCE FROM N.A.
MEDLINE=93260018; PubMed=7684041;
Fietz M.J., McLaughlan C.J., Campbell M.T., Rogers G.E.;
"Analysis of the sheep trichohyalin gene: potential structicalcium-binding roles of trichohyalin in the hair follicle J. Cell Biol. 121:855-865(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE MOLECULE. DOMAIN 9 CONTAINS THE C-TERMINUS, CONSERV DIFFERENT SPECIES.
PTM: SUBSTRATE OF TRANSGLUTAMINASE. SOME 200 ARGININES PROBABLY CONVERTED TO CITRULLINES BY PEPTIDYLARGININE D SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS
                                                                                                                                                                 Border Leicester; TISSUE=Wool
                                                                                                                                                                                             Fietz M.J., Presland R.B., Rogers G.E.;
"The cDNA-deduced amino acid sequence for trichohyalin, differentiation marker in the hair follicle, contains a repeat.";
J. Cell Biol. 110:427-436(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calcium-binding.
S-100 LIKE.
EF-HAND 1 (LK
EF-HAND 2 (HI
14 X 28 AA 1-1.
                                                                                                                                        SEQUENCE OF 1016-1549 FROM N.A. STRAIN-Merino-Dorset horn X Bord MEDLINE-90130632; PubMed-2298812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A34209; A34209.
PIR; A34209; A34209.
PIR; A40691; A40691.
HSSP; P02633; 11G5.
InterPro; IPR001751; CaBP_S100.
InterPro; IPR002048; EF-hand.
Pfam; PF01023; S_100; 1.
ProDom; PD003407; CaBP_S100; 1.
PROSITE; PS00018; EF_HAND; 1.
PROSITE; PS00303; S100_CABP; FAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP_
JO; 1.
(CaBP_S100; 1
18; EF_HAND; 1.
303; S100_CABP; F?
Repeat; Calc*
91
33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z18361; CAA79165.1; -. EMBL; X51695; CAA35992.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
62
413
413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keratinization;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---
```

```
Gaps
                                                                                  AA APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=13 / Type A;
PubMed=11792842;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic flesh-eater.";
                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                     ACD1_CLOPE STANDARD; PRT; 218 AA.
08XMY2;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative acyl carrier protein phosphodiesterase 1).
Phosphodiesterase 1).
CPE0556.
Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridium.
EVEVSRDHASLGDSETLSQTELRKKERKKRERKF
                                                                                                                                                                                                                                                                                    Best Local Similarity 37.
                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                          418
                                                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE
                                                                                                                                                                                                                                                       Query Match
                           REPEAT
REPEAT
REPEAT
REPEAT
                                                              REPEAT
                                                                          REPEAT
                                                                               DOMAIN
                                                                                           REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                             REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                            SEQUENC
                                                                                                                                                          REPEAT
REPEAT
REPEAT
                                                                                                                                                                           REPEAT
REPEAT
REPEAT
                                                    REPEAT
                                                                     REPEAT
                                                                                       REPEAT
                                                                                                                                                                                            REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                 CLOPE
                                                                                                                                                                                                                                                                                                           RESULT
```

ö

g

15:44:2

9

Wed Jul

.rsp

586

Ŧ 3

54-13

us-09-8

```
collaboration
                                                                                                                                                           way
                                                                                                                                                                        commercial
                                                                                                                                                                                     sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                          100
                                                                                                                                                                                                                                                                                                                                                            --HASLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWI 48
                                                                                                                         tics and the EMBL outstation
ere are no restrictions on it
as its content is in no was
Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                       157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rat
                                                                                                                                                                                                                                                                                                                                                                                           KNADLYVIAAP
                                                                                                                                                                                                                                                                                                                                                                                                                         GCLPWATR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (5-HT7) receptor gene: genomic organization a reening in schizophrenia and bipolar affective
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   man and rate to altered
                    cleavage of similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rietschel M.,
rner J., Weigelt B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             | :|| |:
GEIPWLTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ostomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor (5-HT7) positively
                                                                                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Α.,
                                                                                                              Ø
                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECI
MEDLINE=97238071; PubMed=9084407;
Heidmann D.E.A., Metcalf M.A., Kohen R., Hamblin M.W.;
"Four 5-hydroxytryptamine7 (5-HT7) receptor isoforms in hu
produced by alternative splicing: species differences due
intron-exon organization.";
J. Neurochem. 68:1372-1381(1997).
FUNCTION: Acad. Sci. U.S.A. 99:996-1001(2002).

FUNCTION: Converts holo-ACP to apo-ACP by hydrolytic class phosphopantetheine prosthetic group from ACP (By State of Activity: Holo-[acyl-carrier protein] + H(2)(phosphopantetheine + apo-[acyl-carrier protein].

SIMILARITY: BELONGS TO THE ACPD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                           41 EVDLYKDFIPRLEHKHFSGRSSVVDCETASIDAKTKEEVKRIIELSEQF
                                                                                                                                                                                                                                                                                                                                                                                                                                             (Serotoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutele
                                                                                                             through
                                                                                                                                                                                                                                                                                                21
                                                                                                                                                                                                                                                                                                                                                                                                                           --TG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ithe European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adham N., Vaysse P., Branchek
                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                               Hydrolase; Complete proteome.
1965 MW; 82E54E1A03EE253F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           --TCREML--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Korner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5H7_HUMAN STANDARD; PRT; 479 AA. P34969; P78516; P78336; P78372; 01-FEB-1994 (Rel. 28, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 5-hydroxytryptamine 7 receptor (5-HT-7) (5-HT-X)
                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANTS LYS-92 AND LEU-279.
MEDLINE=97298817; PubMed=9154233;
Erdmann J., Nothen M.M., Shimron-Abarbanell D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Erdmann J., Nothen M.M., Shimron-Abarbanell I Albus M., Borrmann M., Maier W., Franzek E., Fimmers R., Propping P.; "The human serotonin 7 (5-HT7) receptor gene: systematic mutation screening in schizophrenidisorder."; Mol. Psych. 1:392-397(1996).
                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           -IQESLLCPPSPKEV--
                                                                                                                                                                                                                                                                                                Score 61.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268:23422-23426(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serotonin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM A).
TISSUE=Placenta, and Fetal brain;
MEDLINE=94043137; PubMed=8226867;
Bard J.A., Zgombick J.M., Adham N
                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                  AP003187; BAB80262.1; -, hetical protein; Hydrolas NCE 218 AA; 24965 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adenylate cyclase.
                                                                                                                                                                                                                                                                                                11.6%;
24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           novel human
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           49 FWILLFSHHW--
                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                             1 EVEVSRD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bard J.A., Zgomb
Weinshank R.L.;
"Cloning of a no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chem.
                                                                                                                                                                                                                                                 Hypothetical
SEQUENCE 2:
                                                                                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linked to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol.
                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                    EMBL;
       Proc.
                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTR7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SULT
                                                                                                                                                                                                                                                                                                                 Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                            ğ
                                                                                                                                                                                                                                                                                                                                                              ŏ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISSING (IN ISOFORM B).
RACTRRVLLRPEKRPPVSVWVLQSPDHHNWLADKMLTTVEK
                                                                                             SUBCELLULAR LOCATION: Integral membrane protein.

ALTERNATIVE PRODUCTS: 3 ISOFORMS; D (SHOWN HERE), A AND B; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORM D IS THE LONGEST ISOFORM BUT ISOFORMS A AND B APPEAR TO BE EXPRESSED AT HIGHER LEVELS.

TISSUE SPECIFICITY: ISOFORM A IS THE PREDOMINANT ISOFORM IN SPLEEN, CAUDATE AND HIPPOCAMPUS. ISOFORM B IS EXPRESSED AT LOWER LEVELS, AND ISOFORM D IS A MINOR ISOFORM.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATE ADENYLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein;
Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 POTENTIAL.

EXTRACELLULAR (POTENTIAL).
5 POTENTIAL.
CYTOPLASMIC (POTENTIAL).
6 POTENTIAL.
EXTRACELLULAR (POTENTIAL).
7 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).

1 POTENTIAL.

CYTOPLASMIC (POTENTIAL).

2 POTENTIAL.

EXTRACELLULAR (POTENTIAL).

3 POTENTIAL.

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VAR_012996.
1F62E985EADE1F23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ~ ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IN ISOFORM B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIA
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
BY SIMILARITY.
PALMITATE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VAR_012995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.5; I
No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane;

Multigene family; Lipoprotein; Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53554 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.6%;
29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                         AAB48393.1;
AAB48394.1;
AAF07218.1;
AAF07217.1;
AAB48397.2;
AAB48397.2;
AAB48397.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:5302; HTR7
MIM; 182137; -.
InterPro; IPR000276; G
Pfam; PF00001; 7tm_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity
25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 1054
1 1058
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 1139
1 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92
                                                                                                                                                                                                                                                                                                                                                                                                                             U68487;
U68488;
U68492;
U68493;
U68492;
U68493;
U68492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymorphism.
                                                                                CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                           THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
```

δ

5

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collaboration
                       LLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHORT
                                                                                                                                                                                                                                                                                                                                                                                                     a gene from Rhizobium melilotii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Batut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        loux 8
D.,
r U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRIN=1021;

MEDLINE=21396507; PubMed=11481430;

Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.";

Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

-!- FUNCTION BINDS MRNA; THUS FACILITATING RECOGNITION OF THE INTIATION POINT. IT IS NEEDED TO TRANSLATE MRNA WITH A SHC SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).

-!- SIMILARITY: CONTAINS 6 SI MOTIF DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ъ.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE
                                                                                                                                                                                                            Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae; Sinorhizobium.
NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
01-JAN-1990 (Rel. 13, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
30s ribosomal protein S1.
RPSA OR R00255 OR SMC00335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA-binding; (S1 MOTIF 1. S1 MOTIF 2. S1 MOTIF 3. S1 MOTIF 4. S1 MOTIF 5.
                                                                            370
                                                                                                                                                                                                                                                                                                                                                                 Schnier J., Thamm S., Lurz R., Hussain Dobrinski B.; "Cloning and characterization of a gene coding for ribosomal protein S1."; Nucleic Acids Res. 16:3075-3089(1988).
                                        EMBL; AL591783; CAC41692.1; -. PIR; S01055; R3ZR1. HSSP; P05055; 1SRO. InterPro; IPR000110; Ribosomal_S1 InterPro; IPR003029; S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00575; S1; 6.

FS; PR00681; RIBOSOMALS1.

F; SM00316; S1; 6.

FMS; TIGR00717; rpsA; 1.

FTE; PS50126; S1; 6.

Somal protein; Repeat; RN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAA30404.1; -
3; CAC41692.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat;
93
177
266
353
440
                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                           FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111
198
283
370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X07528;
                                                                                                                                               RS1_RHIME
P14129;
                                                                        348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGRFAMS;
                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF
PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                          Q
                                                                       d
```

```
ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           þe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       novirus 89 (HRV-89).
ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLG_HRV89 STANDARD; PRT; 2164 AA.
POLG_HRV89 STANDARD; PRT; 2164 AA.
POLG_HRV89 STANDARD; Q82098; Q82099; Q82100; Q82101; Q82102;
Q82103; Q82104; Q82105;
Q82103; Q82104; Q82105;
Q82103; Q82104; Q82105;
Q1-APR-1988 (Rel. 07, Created)
O1-APR-1988 (Rel. 07, Last sequence update)
O1-APR-1988 (Rel. 07, Last sequence update)
I5-JUN-2002 (Rel. 41, Last annotation update)
Genome polyprotein [Contains: Coat proteins VP1 TO VP4; Core protein P2A TO P2C, P3A; Genome-linked protein VPG; Picornain 3C
(EC 3.4.22.28) (Protease 3C) (P3C); RNA-directed RNA polymerase P3D (EC 2.7.7.48)].
Human rhinovirus 89 (HRV-89).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND VP4.
SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               poliovirus polyprotein. In other picornavirus reactions Glu masubstituted for Gln, and Ser or Thr for Gly.

CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duechler M., Skern T., Sommergruber W., Neubauer C., Gruendler P Fogy I., Blaas D., Kuechler E.; "Evolutionary relationships within the human rhinovirus genus: comparison of serotypes 89, 2, and 14."; Proc. Natl. Acad. Sci. U.S.A. 84:2605-2609(1987).

-!- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTY Q/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.

-!- CATALYTIC ACTIVITY: Selective cleavage of Gln-|-Gly bond in poliovirus polyprotein. In other picornavirus reactions Glu r substituted for Gln, and Ser or Thr for Gly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {RNA}(N).
SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNIT;
EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1,
                                                                                                                                                                                                                                                                          ij
                                                        -> ADAQPAALRN (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
3
                                                                                                                                                                                                                                                                                                                                                                                 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY
                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                   EVEVSRDHASLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIF
                                                                             -> K (IN REF. 1).
-> Q (IN REF. 1).
-> R (IN REF. 1).
AB0858204273A7B8 CRC64;
                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                        DB
                          A -> R (IN REF
LMHNPQPFEI -> 1
                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                  Score 61.5; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cys-protease-3C.
Pico_PlA.
Pico_P2A.
Pico_P2B.
RNA_helicase.
                                                                                \ \ \
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87204179; PubMed=3033653
                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M16248; AAA45762.1; -.
EMBL; A10937; CAA00931.1; -.
PIR; A29862; GNNY89.
MEROPS; C03.007; -.
MEROPS; C03.021; -.
InterPro; IPR000199; Cys-proteinterPro; IPR003138; Pico_P1A.
InterPro; IPR000081; Pico_P2A.
InterPro; IPR000605; RNA_helicalInterPro; IPR001205; RNA_helicalInterPro; R
                                                                                                                                                            62640 MW;
                                                                                                                                                                                                                 11.6%;
37.0%;
                                                                                                                                                                                                                                                                  Conservative
530
88
162
235
241
551
                                                                                                                                                            AA;
                                                                                                                                                                                                                                          Similarity
17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=12132;
 459
88
153
235
241
551
                                                                                                                                                            89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhinovirus
                                               CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses;
                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                  Query Match
                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VP3,
PTM:
                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OLG_HRV89
                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>-</u>:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                               FT
FT
FT
                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
```

```
1919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -CPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVTGSAVGCDPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pediococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=PAC-1.0; PLASMID=pSRQ11;
MEDLINE=92384551; PubMed=1514784;
Marugg J.D., Gonzalez C.F., Kunka B.S., Ledeboer A.M., Pucci M.J.,
Toonen M.Y., Walker S.A., Zoetmulder L.C.M., Vandenbergh P.A.;
Toonen M.Y., walker S.A., and nucleotide sequence of genes involved in
production of pediocin PA-1, and bacteriocin from Pediococcus
acidilactici PAC1.0.";
Appl. Environ. Microbiol. 58:2360-2367(1992).
                                                                                                                                                                                                                                     ristate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                P3D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ing
                                                                                                                                                                                                                                                                                                                                                                                                           3B)
                                                                                                                                                                                                                                     Σ
                                                                                                                                                                                                                                                                                                                                                                                                          (P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=H; PLASMID=pSMB74;
MEDLINE=94288967; PubMed=7764941;
Motlagh A.M., Bukhtiyarova M.B., Ray B.R.;
"Complete nucleotide sequence of pSMB 74, a plasmid encodificon production of pediocin AcH in Pediococcus acidilactici.";
Lett. Appl. Microbiol. 18:305-312(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLSQTELRKKER-KKKRERKFQANCGIDFIIFWIFWILLFSHHWIQES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TFLKDELRKKEKIKDGKTRVIEANSVNDTVLFRSVFGNLFSAFHKNPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Bacteriocin pediocin PA-1 precursor (Pediocin ACH).
PEDA OR PAPA OR PAP.
Pediococcus acidilactici.
Plasmid pSRQ11, and Plasmid pSMB74.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                        GENOME-LINKED PROTEIN VPG (PPICORNAIN 3C.
RNA-DIRECTED RNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                   protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYRISTATE (BY SIMILARITY)
                                                                                                                                                                                                                   se
                                                                                                                                                                                                                                                                     (P1B).
(P1C).
(P1D).
                                                                                                                                                                                                                   ransfera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEASE (POTENTIAL).
PROTEASE (POTENTIAL).
W; F5D9C8F4FBEA7D54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               re 61.5; DB 1;
dd. No. 1.1e+02;
Mismatches 35;
                                                                                                                                                                                                                                                                                                                           CORE PROTEIN P2A.
CORE PROTEIN P2B.
                                                                                                                                                                                                                                                                     VP2
VP3
VP1
                                                                                                                                                                                                                                Hydrolase; Thiol
COAT PROTEIN VP4
                                                                                                                                                                                                                                                                      COAT PROTEIN
COAT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                          CORE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPA1_PEDAC Similar PPA1_PEDAC Similar P29430; P34912; 01-APR-1993 (Rel. 25, Created) 01-JUN-1994 (Rel. 29, Last sequence upda 01-JUN-2002 (Rel. 41, Last annotation upda 17 TIN-2002 (Rel. 41, Last a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                 PD001125; Cys-protease-3C;
PD001274; Pico_P2B; 1.
PD001306; Pico_P2A; 1.
Stein; Coat protein; Core pro
               ; PF00073; rhv; 3.
; PF00073; rhv; 3.
; PF00548; Cys-protease-3C; 1;
; PF00680; RNA_dep_RNA_pol; 1;
; PF00910; RNA_helicase; 1.
;; PF01552; Pico_P2A; 1.
;; PF01552; Pico_P2B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MΨ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.6%;
larity 32.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKEVTCREMLTGGCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VFWSTIPLMLDGECL
                                                                                                                                                                                                                                                     2336
3369
3366
11008
11103
11424
11521
11521
11668
11668
Pro; IPR001676; R|
PF00073; rhv; 3.
PF00548; Cys-pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 24; Conser
                                                                                                                                                                                                                                                                     70
337
575
867
1009
1104
1152
1522
1705
1682
2168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1254
                                                                                                                                                                                                               Polyprotein;
RNA-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16
                                                                                                                                                                                              ProDom;
                                                                                            Pfam; PE
Pfam; PE
Pfam; PE
ProDom;
                                                                                                                                                                        ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appl.
[2]
                                                                                                                                                                                                                                                                     CHAIN
CHAIN
CHAIN
CHAIN
CHAIN
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
CHAIN
CHAIN
LIPID
                                      Pfam;
                                                                             Pfam;
                                                          Pfam;
                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PA1_PEDAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SULT
                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            뒫
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DE
GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                  LISTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
Murinae; Mus
                                                                                                                         ρλ
                                                                                                                                                                                                                                                                               Pelaz C., Nes I.F.;
f a bacteriocin produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
                                                                                                                          produced
                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO BACTERIOCIN CLASS IIA/YGNGV FAMILY
                                                                                                                                                                                                                                                                                                                                                                                    O.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-89042086; PubMed-2847145;
Watson D.K., McWilliams M.J., Lapis P., Lautenberger J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 62;
                                                                                                                                                                                                                        SEQUENCE OF 19-61.
MEDLINE=93019000; PubMed=1402795;
Lozano J.C.N., Meyer J.N., Sletten K., Pelaz C., Nes I.F.
"Purification and amino acid sequence of a bacteriocin pr
Pediococcus acidilactici.";
J. Gen. Microbiol. 138:1985-1990(1992).
-:- FUNCTION: BACTERICIDAL ACTIVITY (EFFECTIVE INHIBITOR MONOCYTOGENES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACTERIOCIN PEDIOCIN PA-1 HYDROPHOBIC.
[3]
SEQUENCE OF 19-62, AND DISULFIDE BUNCS.
STRAIN=PAC-1.0; PLASMID=pSRQ11;
MEDLINE=92246549; PubMed=1575516;
Henderson J.T., Chopko A.L., van Wassenaar P.D.;
"Purification and primary structure of pediocin PA-1
Pediococcus acidilactici PAC-1.0.";
Pediococcus acidilactici PAC-1.0.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8E6F10D49FA87BA9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               468 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M83924; AAA25559.1; -.
EMBL; M90679; AAA98337.1; -.
EMBL; U02482; AAC43293.1; -.
PIR; A41823; A41823.
PIR; A41823.
PIR; A48941; A48941.
PIR; A47680; A47680.
HSSP; P34034; 2LEU.
InterPro; IPR002633; Bacteriocin_II.
Pfam; PF01721; Bacteriocin_II; 1.
ProDom; PD004452; Bacteriocin_II; 1.
Antibiotic; Bacteriocin; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 KEVICREMLIGGCLPWAIRSHLGRRKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.5%;
40.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6644 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 14, (Rel. 14, 1) (Rel. 14, 1) (Rel. 40, 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Wonse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-ETS-2 protein ETS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
40
42
42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990
01-APR-1990
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETS2_MOUSE P15037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T 14
MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
ETS2_MC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCOUNT OF THE STANDARY OF THE
                                                                                                                                                                                                                                                                                                                                                          SHTTTTT SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qγ
```

1;

```
h a collaboration EMBL outstation
                                                                                                                                             is in no way
d for commercial
sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                    outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
                                                                                            This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KERKKKRERKFQANCGIDFIIFWIFWILL-FSHHWIQESLLCPPSPKEVTCREMLTGGCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --NLLDSMCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                       roteins."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=86181601; PubMed=3008427;
Dartmann K., Schwarz E., Gissmann L., Zur Hausen H.;
"The nucleotide sequence and genome organization of human papilloma virus type 11.";
Virology 151:124-130(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 KENQEKTEDQYEENSHLNAVPHWINSNTLGFSMEQAPYGMQAPNYPKD-
                       conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probable E4 protein.
Human papillomavirus type 11.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                                                     Schweinfest C.W., Papas T.S.;
"Mammalian ets-1 and ets-2 genes encode highly control at l. Acad. Sci. U.S.A. 85:7862-7866(1988)
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE ETS FAMILY.
-!- SIMILARITY: CONTAINS 1 POINTED (PNT) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 02, Created)
(Rel. 02, Last sequence update)
(Rel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 60.5; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 29;
12; Mismatches
                                                                                                                                                                                                      EMBL; J04103; AAA37581.1; -. PIR; C32066; TVMSE2.
HSSP; P14921; 2STT.
TRANSFAC; T01397; -. MGD; MGI: 95456; Ets2.
InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS.
InterPro; IPR002341; HSF_ETS.
InterPro; IPR003118; SAM_PNT.
Pfam; PF00178; Ets; 1.
Pfam; PF02198; SAM_PNT; 1.
PRINTS; PR00454; ETSDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.4%;
Similarity 29.0%;
0; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 PSATPAALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PWATRSHLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Papillomavirus.
NCBI_TaxID=10580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VE4_HPV11
P04016;
23-OCT-1986
23-OCT-1986
01-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
VE4_HPV11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ά
```

```
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                          2
                                                                                                                                                           Gaps
                                                                                                                                                          14;
                                                                                                                                  Length 108;
                                                                                                                                                         9; Indels
                                                                                                          1B3B77B0DAF7E835 CRC64;
                                                                                                                                                                                                      85
                                                                                                                                                                                --PWATRS 89
                                                                                                                                                                                           DB 1;
                                                                                                                                              ed. No. 7;
Mismatches
                                                                                                                                                                                --LTGGCL---
                                                                                                                                           7;
                                                                                                                                 Score 60;
Pred. No.
                                                        PIR; A03675; W4WL11.
InterPro; IPR003861; Papilloma_E4
Pfam; PF02711; Pap_E4; 1.
Early protein.
SEQUENCE 108 AA; 12144 MW; 1B:
                                                                                                                                                       5;
                                                                                                                               th 11.3%;
Similarity 31.7%;
13; Conservative
                                                                                                                                                                               63 LLCPPSPKEVTCREM--
                                               EMBL; M14119; AAA46931.1;
                                                                                                         108 AA;
                                                                                                                                Query Match
Best Local S
Matches 13
 q
                                                                                                                                                                               ŏ
```

2003, 15:08:48

6

Search completed: July Job time: 16.0177 secs

Job time

```
updates/sec
                                                                               US-09-854-133-586
532
1 EVEVSRDHASLGDSETLSQT.....LTGGCLPWATRSHLGRRKCS 97
                                                econds
                                               ; Search time 43.7788 Se (without alignments) 456.536 Million cell
                                                                                                                                                          671580
5.1.6
Compugen Ltd.
                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                         671580 seqs, 206047115 residues
version - 2003
                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                - protein search, using sw model
                                                                                                                                                                                                                                       2003, 15:05:28
                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
GenCore
Copyright (c) 1993
                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                   SPTREMBL_21:*
                                               6
                                               July
                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                 Scoring table:
                                OM protein
                                                                                                Sequence:
                                                                                                                                         Searched:
                                                                                                                                                                                                                                   Database
                                                Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	O96ex2 homo sapien	2 vibr	Q9m896 arabidopsis	011498 human immun	O11503 human immun	Oll505 human immun	Q9u0q5 plasmodium		O11502 human immun	Oll504 human immun	Q9yiw8 human immun	Q9epj7 mus musculu	Q8uqb2 human immun	Q9u418 branchiosto	Q18657 caenorhabdi	Q8uqa8 human immun
ΙĐ	096EX2	Q9KNH2	968M60	011498	011503	011505	Q900G5	016652	011502	011504	O9YIW8	09EPJ7	Q8UQB2	Q9U418	Q18657	Q8UQA8
DB	4	16	10	15	15		5	2	15	15	15	11	15	2		15
Length	231	177	373	396	396	396	2277	684	396	396	353	463	169	411	1851	169
% Query Match	5.	13.6	т •	ж.	ж •	ω,	ω,	ش	.	ж •	8	ς.	ς.	2	~	, ,
Score	ŧ	72.5	72									68	67.5	•		999
Result No.	1	7	ო	4	5	9	7	ω	თ				13			

O96296 plasmodium	Q9fz10 phaseolus v	9vdj6 (drosophi	9vrr0 (_	human	' human i	oryza	Q90s38 chimpanzee	human,	drosophi	8swq1 encepha	human	_	clostr		arabidops	9txp5 (chloro	oryza	Ü	human	Q8uqb1 human immun	mus mu	i human i	_	schizosa	Q9wmu7 human immun	(2	
096296	Q9FZ10	09VDJ6	061730	Q9VRR0	Q8UQC1	Q8UQC9	Q80QD7	Q8S1H7	090838	089607	Q9W248	Q8SWQ1	Q8UQB5	093081	Q8XNM5	094456	Q8S2T0	Q9TXP5	046472	Q94DU0	Q9Y7E0	Q8UQB3	Q8UQB1	099163	Q9WEG5	Q99P01	Q9P3U8	Q9WMU7		ALLGNMENTS	
2	10	Ŋ	Ŋ	Ŋ	15	15	15	10	15	15	Ŋ	S			16			Ŋ	7	10		15					m	15			
9	9	3	3	ϵ	7	6	Φ	9	근	2	3	O	9	~	\sim	8	æ	σ	0	7	œ	9	9	$^{\circ}$	9	~	468	0			
2	2	7	2	ς.	ς.	2	2	2	2	2	ς.	5	5	2	4.	ά.	7	5	ς.	S.	ς.	ij.	-	;	;	H	11.9	۲,			
	Ō										9	4	4	4	•	4.	4.	9	9	Ó	Ó	Э.	ж Э	ж Э	<u>.</u>	ж Ж	63.5	Э.			
																											44				DECTIT 1

										m	52	207			
			1;							Gaps	EVSRDHASLGDSETLSQTELRKKERKKKRERKFQANCGIDFI-IFWIFWIL	:: :: : : : : ::		•	
			Euteleostomi; Homo.							10;	I - IE	; VSCL			
			Sutelec Homo.				ro			231; 1s	CGIDE	CGYPI			
	_		; Eu e; He			,	base		C64;	Length 231;	FQAN	LWPR			
	ite) date		orata Inida			,	data		C CR	Length 23.	KRERK	KKAQ			
AA.	upda		ertek Homj				DDBJ		b3C57	DB 4; 0.047; ches 1	ERKK	H:: GRKEF			AA.
231 AA.	Created) Last sequence update) Last annotation update)	627.	Craniata; Vertebrata; Catarrhini; Hominidae;			•	the EMBL/GenBank/DDBJ databases); CYTOCHROME_C; UNKNOWN_1. A; 25722 MW; B4D36B0360D3C57C CRC64;	Score 84; DB Pred. No. 0.04	RKK	II: GRKE			177
ľ;	red) segu	FLJ14	aniat tarrk			!	/GenE	ind.	UNKNC 4D36E	Score 84; Pred. No.		ERREC			: ` ⊟
PRT;	Created) Last seq	protein FLJ14627.					EMBL,	Cytc_heme_bind.	C; B	Scor Pre(TEL-	: KKKK			PRT;
	19,	1.1	Chordata; Primates;			•	the	c_he	IROME	15.8%; 31.2%; ive 1	TLSO	TLSK			
IMINARY;	MBLrel. MBLrel. MBLrel.	ical					001) to the AAH11878.1:	; Cyt	YTOCE 2572	15, 31, ative	DSI	I II DRVSE			IMINARY;
	(Tremblrel.	hypothetical	zoa; ria;		. A.				0; C	15.8 larity 31.3 Conservative	ASLG	SNLG	26	211	
PREL		pypo		NCBI_TaxID=9606;	ROM N	ж ;;	tted (JUL-2 BC011878:	IPR00	PS00190; 231 AZ	Similari O; Cons	VSRDH	:: IAPQH	LFSH 5	LFCH 2	PREL
	-2000 -2000	ar to h	ota; ia; I	axID	CE FI =MUS(berg	ted BC01.	,		요 2	т Н	148 E	53 L)	208 L	••
T 1 2 Q96EX2	Q96EX2; 01-DEC-2001 01-DEC-2001 01-MAR-2002	Similar Homo sa	kary mmal	BI_T	SEQUENCE FROM TISSUE-MUSCLE:	Strausberg	Submitted EMBL: BCO	InterPro;	PROSITE; SEQUENCE	Match Local				7	.T 2 12 Q9KNH2 Q9KNH2;
RESULT Q96EX2 ID Q9	0000	Si	En Ma	NCB	SE	St	SU	ü	PF	Query M Best Lo Matches					RESULT Q9KNH2 ID Q9 AC Q9
RES O96 ID	DI	DE	888	N N	RP RC	RA	RI DR	DR	DR SQ	<u> </u>	Qγ	qq	QY	OD	RES 099 ID

```
320 NITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
Balotta C., Ri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MLTG
                                                                                                                               011498
011498;
01-JUL-1997
01-JUL-1997
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              011503;
011503;
01-JUL-1997
01-JUL-1997
                                                 65
                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
     5
                                                                         136
                          97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                              TER
                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                    AIDS;
NON_I
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENA
                                                                                                          4
                                                                                                          RESULT
                                                                                                                    011498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     011503
                                                                                                                                           d
                                                                         d
                                                                                                                                                                                                                                                                      RA
RT
RT
DR
DR
DR
FT
                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                             ij
                                                                                                                                                                             Р.,
                                                                                                                                                                                                   Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                D.,
Sellers D
White O.
                                                                                                                                            M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ence.";
                                                                       Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosi
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wu D
M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ω
                                                                                                                                                       L.A.,
                                                                                                                                                                                                                          Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=EL TOR N16961 / SEROTYPE 01;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.P. Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Oin H., Dragoi I., Sel McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., Whish Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter Fraser C.M.;

"DNA sequence of both chromosomes of the cholera pathogen Vibration."
                                                                                                                                             inn
                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC F16B3 genomic seque
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC021640; AAF32451.1;
InterPro; IPR004253; DUF231.
R Pfam; PF03005; DUF231; 1.
SEQUENCE 373 AA; 43367 MW; 76DF8859CBF950A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          : ::| | | :| || :::|
LKQEHEKKVDVEVISATELSEQQRSEIGSKLEQRLERKVQLNCSVD 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barnstead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sedn
                                                                     Proteobacteria; gamma subdivision; Vibrionaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haas B
                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  ---KKKRERKFQANCGID
                                                                                                                                                                                                                                                                                                                                                              218356C3B0937D52 CRC64;
(TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                                                   Score 72.5; DB Pred. No. 0.87; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 72;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                             Н
                                                                                                                                                                                                                                                                                                   PRINTS; PR00125; ATPASEDELTA.
TIGREAMS; TIGR01145; ATP_synt_delta;
PROSITE; PS00389; ATPASE_DELTA; 1.
Complete proteome.
SEQUENCE 177 AA; 19558 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                4 VSRDHASLGDSETLSQTELRKKER---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                        IPR000711; ATPsynt_OSCP
0213; OSCP; 1.
                                    subunit.
                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                  13.6%;
32.6%;
                                                                                                                                                                                                                                cholerae.";
Nature 406:477-483(2000).
EMBL; AE004342; AAF95906.1;
HSSP; P00831; 1ABV.
TIGR; VC2767; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15,
15,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.5%;
larity 30.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                   delta
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
ses 15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 23; Conservation
                                   ATP synthase F1, VC2767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protėin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eurosids II; Bra
NCBI_TaxID=3702;
                                                        Vibrio cholerae
                                                                                 NCBI_TaxID=666;
 01-OCT-2000
01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9M896;
01-OCT-2000
01-OCT-2000
01-JUN-2002
                                                                    Bacteria;
                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                      66
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F16B3.7
F16B3.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             968M60
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                               Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 968M60
                                                                   ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC
DT
                                                                                                                                                                                                                                                                                                                                                                                                                                à
```

4;

Gaps

28;

Indels

18;

Mismatches

7;

```
4,
                                  135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16
64
                                                                                                                                                                                                                                                                                                                                                                                                            Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ø
 SRDHASLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWIFWILLFSHHWIQESLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - IQESLLCPPSPKEVTCRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 YCNTTQLFNSTWNVTEGLNNTEGNDTIILPCRIKQIINMWQEVGKAMYAPPISGQIRCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                  -FSGEWI
                                                                                                                                                                                                                                                                                                                                                                                           Moroni M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moroni M.
                                                                                                                                                                                                                                                                                                                                                                                     Balotta C., Riva C., Violin M., Colombo C., Galli M., Moroni M. "Analysis of the V1-V5 env region in Long-Term Non Progressor rapid progressor infected individuals.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U95401; AAB52747.1; -.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Balotta C., Riva C., Violin M., Colombo C., Galli M., Moroni M. "Analysis of the V1-V5 env region in Long-Term Non Progressor rapid progressor infected individuals.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U95406; AAB52752.1; -.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus NCBI_TaxID=11676;
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             457EC5D0CA1A9E54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         th 13.5%; Score 72; DB 15; Similarity 20.2%; Pred. No. 2.2; 25; Conservative 19; Mismatches 32;
                              --cDi
                                                                                                                                                                                                                    (TrEMBLrel. 04, Created)
(TrEMBLrel. 04, Last sequence up
(TrEMBLrel. 19, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     396 AA
                                                                                                                                                                                      396
                  Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                      Envelope glycoprotein (Fragment) ENV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44103 MW;
                                                                75
                                                                                       --PNPKAPYYTNTTCR
                                                                   --EVTCR
                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WIEWILLFSHHW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396
396 AA;
                                                                 CPPSPK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323
```

5

711

78

```
4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9/
                                                                                                      46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPPSPKEVTCRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 YCNTTQLFNSTWNVTEGLNNTEGDDTIILPCRIKQIINMWQEVGKAMYAPPISGQIRCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --NCGIDFILF
                                                                                                                                                   --IQESLLCPPSPKEVTCRE
                                                                                                                             - - F
                                                                                                                                                                         260 YCNTTQLFNSTWNVTEGLNNTEGNDTIILPCRIKQIINMWQEVGKAMYAPPISGQIRCSS
                                                                                                                                                                                                                                                                                                                                                                                                                    Balotta C., Riva C., Violin M., Colombo C., Galli M., Moroni M.; "Analysis of the V1-V5 env region in Long-Term Non Progressor and in rapid progressor infected individuals."; Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U95408; AAB52754.1; -. InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Glycoprotein.
                                                                                                       --NCGIDFIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                Gaps
                                                                                                                   48;
                                                                                48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    396;
                                                        396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---IQESLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EF6AD3F0B027FB21 CRC64;
                                  1F7EC53DB27A8669 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                  01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUC-2001 (TrEMBLrel. 19, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 EVSRDHASLGDSE---TLSQTELRKKERKKKRERKFQA-
                                                                                32;
                                                                                                       3 EVSRDHASLGDSE---TLSQTELRKKERKKKRERKFQA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.5%; Score 72; DB 15;
larity 20.2%; Pred. No. 2.2;
Conservative 19; Mismatches 32
                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2277 AA
                                                                                                                                                                                                                                                                                   396 AA
                                                        Score 72; DB
Pred. No. 2.2;
19; Mismatches
                                                                                                                                                                                                                                                                                   PRT;
Coat protein; Glycoprotein
                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44120 MW;
                                  44050 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09U0G5;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
Var, MAL4P2.58.
                                                          13.5%; 20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WIFWILLFSHHW----
                                                                                Conservative
                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY
                                                                                                                                                       WIEWILLFSHHW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396
396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 25; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                 N.A.
                       396
396 AA;
                                                                    Similarity
25; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 NITG 323
                                                                                                                                                                                                                          323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 MLTG 80
                                                                                                                                                                                                   77 MLTG 80
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                          320 NITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
                        NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
                                                                                                                                                                                                                                                                                  011505
011505;
            NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q900G5
  AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                            RESULT
011505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q900G5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC
DT
DT
DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RL
DR
DR
DR
FT
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
    KY
FT
SO
                                                                                                                               d
                                                                                                                                                                             d
                                                                                                                                                                                                                          d
                                                                                                                                                                                                   ğ
                                                                                                                                                       õ
                                                                                                         δ
```

```
STRAIN=BRISTOL N2;

MEDLINE=94150718; PubMed=7906398;

Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,

Lightning J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,

Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,

Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,

Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

T elegans.";
                                                                                                                                                                                                                                                                                                                  22 LRKK -- ERKKKRERKFQANCGIDFIIFWIFWILLFSHHWIQESLL-CPPSPKEVTCREML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                        Churcher C., Harris B., Harris D., Lawson D.
                                                                                                                                                                                                                                                                 20;
                      Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                   Length 2277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 elegans cosmid T06D4.";
to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the EMBL/GenBank/DDBJ databases
                                                                                                                                       databases
                                                                                                                                                                                                  E4262CCA69DDEF93 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C2A8C605CB007A08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                   5;
                                                                                                                                     tted (FEB-1999) to the EMBL/GenBank/DDBJ
AL035475; CAB62899.1; -.
Pro; IPR004258; PFEMP.
PF03011; PFEMP; 2.
NCE 2277 AA; 256122 MW; E4262CCA69DDE
                                                                                                                                                                                                                                   Score 71; DB 5
Pred. No. 16;
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             739
                                                                                                                                                                                                                                                                                                                                                                                 - PWAT - RSHLGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston R.;
Submitted (JUL-1997) to the EMBL/Ger
EMBL; AF016673; AAB66123.1; -.
InterPro; IPR000718; Peptidase_M13.
Pfam; PF01431; Peptidase_M13; 1.
SEQUENCE 684 AA; 79176 MW; C2A80
            307)
                                                                                                                                                                                                                                                                15;
                (isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05,
05,
21,
                                                                                                                                                                                                                                     13.3%; 23.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. (
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
MAL4P2.58, VAR.
Plasmodium falciparum
Eukaryota; Alveolata;
NCBI_TaxID=36329;
                                                                                                          Devlin K., Bowman S.,
Quail M., Barrell B.;
Submitted (FEB-1999)
EMBL; AL035475; CAB628
                                                                                                           s:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=BRISTOL N2; Le T.T., Goela D.; "The sequence of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                     Similarity 21; Conser
                                                                            SEQUENCE FROM N.A. STRAIN=3D7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                 TGGCL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T06D4.4 protein
                                                                                                                                                                                     PF03011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998
01-JAN-1998
01-JUN-2002
MAL4P2.58, 1
Plasmodium 1
Eukaryota; 1
                                                                                                                                                                       InterPro;
Pfam; PF03
                                                                                                                                                                                                                                                                                                                                                                 79
                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           016652
016652;
                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              016652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RA
RA
RA
RA
RA
RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RT
RL
RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RP
RC
RA
RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RN
RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RC
RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DT COC OC OC OC OC OC OC OC OC OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RY RY RA RA RA RA RA
  GN
OC
OC
OX
OX
OX
RR
RR
RR
DR
DR
DR
SQ
                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | | : : | : : | CNTTQLFNSTWNVTEGLNNTEGNGTITLPCRIKQIMNMWQEVGKAMYAPPIRGQIRCSSN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCGIDFILFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --IQESLLCPPSPKEVTCREM
                                  Gaps
                                                                                                                                                                                                                                                                                                                      and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and in
                                                                                                                                                                                                                                                                                                         M., Moroni M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      i M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Balotta C., Riva C., Violin M., Colombo C., Galli M., Moroni M "Analysis of the V1-V5 env region in Long-Term Non Progressor rapid progressor infected individuals.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U95405; AAB52751.1; -.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 15; Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Balotta C., Riva C., Violin M., Colombo C., Galli M., Moroni "Analysis of the V1-V5 env region in Long-Term Non Progressor rapid progressor infected individuals.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U95407; AAB52753.1;
InterPro; IPR000777; GP120.
       Length 684;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                    FA685770CDCBCFE9 CRC64;
                                                        -NCGIDFILFWIFWILLF
                                                                                                                                                                                      update)
on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                    Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 VSRDHASLGDSE---TLSQTELRKKERKKKRERKFQA-
      5;
   Score 70; DB 5
Pred. No. 6.4;
9; Mismatches
                                                                                                                                                                                    Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 69; DB 1; Pred. No. 5; 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396 AA
                                                                                                                                                                     (TrEMBLrel. 04, Created)
(TrEMBLrel. 04, Last seq:
(TrEMBLrel. 19, Last anno
                                                                                                                                              PRT;
                                                                                                                                                                                                          Envelope glycoprotein (Fragment).
                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                   396
43975 MW;
   13.2%;
31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.0%;
20.3%;
                                                    23 RKKERKKKRERKFQA-
                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 20.3
nes 25; Conservative
                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 IFWILLFSHHW--
               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    396
396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 ITG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTG 80
                                                                                                                                          011502
011502;
01-JUL-1997
01-JUL-1997
01-DEC-2001
                          14;
Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
SEQUENCE
                                                                              œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match
                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   011504;
                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                       ENV
                                                                                                                             011502
ID 01
                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           011504
                                                                                                                                                                                a
                                                    δ
                                                                                                                                                                                                                                                                                                                           RT DR DR DR DR KW KW KW SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DT DT DT OC OC OC OC OC OC OC OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RP
RA
```

```
4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9/
                                                                                                            46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46
                                                                                                                                                                                                                                                                                                                                                                                                               Kavsan V.M.;

Kavsan V.M.;

"Genetic characterization of HIV-1 variants in Ukraine [in Russian].";

Biopolymers & Cell 14:277-285(1998).

EMBL; Y16082; CAA76048.1; -..

EMBL; Y16081; CAA76047.1; -..

InterPro; IPR000328; Env_GP41.

InterPro; IPR000777; GP120.

InterPro; IPR000777; GP120.

Pfam; PF00516; GP120; 1.

Pfam; PF00517; GP41; 1.

AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
                                                                                                                                                     --IQESLLCPPSPKEVTCRE
                                                                                                            -NCGIDFIIF
                                                                                                                    -ESLLCPPSPKEVTCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --NCGIDFIIF
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-UKRAINIAN;
Grebenjuk V.A., Anoprienko O.V., Skorokhod A.S., Marichev I.L.,
                                                                                       48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353;
                                                                 396;
                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                 Length
                                           281C76D80C080D1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BA670EBAC36227C0 CRC64;
                                                                                                                                                                                                                                                                                        (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
                                                                                      32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 EVSRDHASLGD --- SETLSQTELRKKERKKRERKFQA --
                                                                                                         3 EVSRDHASLGDSE---TLSQTELRKKERKKKRERKFQA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33;
                                                               DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 463 AA.
                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.9%; Score 68.5; Dilarity 19.2%; Pred. No. 5.1; Conservative 19; Mismatches
                                                                 Score 69; D. Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Glycoprotein.
NON_TER 1 1
                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353
39278 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                          44074 MW;
                                                               13.0%;
19.4%;
                                                                                                                                                   WIFWILLFSHHW----
                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 WIFWILLFSHHWIQ--
                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                         (Fragment).
                                396
                       1
396
396 AA;
                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      353
353 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 24; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNITG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 EMLTG 80
                                                                                                                                                                                           77 MLTG 80
                                                                                                                                                                                                               320 NITG
                                                                                                                                                                                                                                                                                        01-MAY-1999
01-MAY-1999
01-OCT-2001
                                                                                                                                                                                                                                                                                                                        ENV protein
                                                                                  24;
                                         SEQUENCE
                                                               Query Match
                                                                                                                                                   47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223
                                                                         Local
                                                                                                                                                                                                                                                                                Q9YIWB;
                                                                                                                                                                                                                                                                    Q9YIW8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9EPJ7
                                                                                                                                                                                                                                              RESULT 11
Q9YIW8
ID Q9YIW
                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                     EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9EPJ7
DR
KW
FT
FT
SQ
                                                                                                         δλ
                                                                                                                             g
                                                                                                                                                   δy
                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DR
KW
FT
FT
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
```

```
ري
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444
                                                                                                                                                                                           encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAFHWFAMSSTCYNPFIYCWLNENFRVELKALLSMCQRPPKPQEDRLPSPVPSFRVAWTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKAIHTNNALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - PPSPKEVTCREMLTGGCLPWAT
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                  Parmentier
                                                                                                                                                                                                                                                                                                                                                                                                                                   46;
                                                                                                                                                                               De Moerlooze L., Williamson J., Liners F., Perret J., Parmenti "Cloning and chromosomal mapping of the mouse and human genes the orphan glucocorticoid-induced receptor (GPR83)."; Cytogenet. Cell Genet. 90:146-150(2000).

EMBL; Y19225; CAC19040.1; -.

EMBL; Y19227; CAC19040.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .`
                                                                                                                                                                                                                                                                                                                                                                                                         463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGDVTTEQYLALR ---RKKKTTVKMLVLVVVLFALCWFPLNCYVLLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Changes in the virus population in acute HIV-1 infection Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF418721; AAL72834.1; -. InterPro; IPR000777; GP120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=93USPIC1008EB3Y;
Muthui D., Brodie S.J., Learn G.H., Zhu T., Diem K., Mull
Corey L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLGDSETLSQTELRKKERKKKRERKFQANCGIDFIIFWI---FWILL-
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271ABB2048D48A6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
EPJ7;
-MAR-2001 (TrEMBLrel. 16, Created)
-MAR-2001 (TrEMBLrel. 16, Last sequence update)
-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                        UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   41;
                                                                                                                                                                                                                                                                                                                                                                               BBC7E96FBB717CE0
                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 68; DB 1
Pred. No. 7.6;
1; Mismatches
O9EPJ7;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence v
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Glucocorticoid induced receptor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169
                                                                                                                                                                                                                                                                                                                             G_PROTEIN_RECEP_F1_1;
G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-129SV;
MEDLINE-20515601; PubMed-11060465;
                                                                                                                                                                                                                                                                                       GPCR_Rhodpsn
                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18687 MW;
                                                                                                                                                                                                                                                                                                  Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN
PROSITE; PS00237; G_PROTEIN_RI
PROSITE; PS50262; G_PROTEIN_RI
                                                                                                                                                                                                                                                                                                                                                                     463
52804 MW;
                                                                                                                                                                                                                                                                                                                                                                                                         12.8%;
larity 22.8%;
Conservative 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21, Envelope glycoprotein gpl20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSHHWIQESLLC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GP120;
                                                                                                                                                                                                                                                                        MGI:95712; Gpr83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169
169 AA;
                                                                                                                                                                                                                                                                                                                                                                    463
463 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
29; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSHLGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSH-GRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            445
                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54
                                                                                                                                                                                                                                                                                                                                                         Receptor
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                      TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8UQB2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8UQB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                            MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                      NON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8UQB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DT DT DT OC OC OC OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RP
RA
RA
RT
                                                                                                                                          DR
DR
KW
FT
SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ф
 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
```

```
4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328
                                                                                105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                      46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---IDFI-IFWIEWILLFSHHWIQ
                                                                       oda; Chromadorea; Rhabditida; Rhabditoidea; Caenorhabditis.
                                                      -NCGIDFIIF
                           Gaps
                                                                                                                                       158
                                                                                                             80
                                                                                                                                                                                                                                                                                              branchiostoma belcheri (Amphoxius).
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
Branchiostoma.
                                                                                                                            : ::: || ::|| :|| 106 YCNTTQLFNSTWNGTVTLPCRIKQIVNMWQEVGKAMYAPPIQGQITCSSNITG
                                                                                                           - IQESLLCPPSPKEVTCREMLTG
                          37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                            genes encodinion in lancelets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                           Indels
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Yasui K., Saiga H., Uemura M., Semba I.;
Yasui K., Saiga H., Uemura M., Semba I.;
"Early body formation and expression pattern of genes er
secreted proteins, BbBMP2/4, BbWnt7, and BbWnt8 in lance
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
-! SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL; AF206325; AAF19841.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Bone morphogenetic protein 2/4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
                           34;
DB 15;
                                                        EVSRDHASLGDSE---TLSQTELRKKERKKKRERKFQA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F579898060F18355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 DHASLGDSETLSQTELRKKERKKKRERKFQANCG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1851 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 67.5; Di
Pred. No. 7.8;
                                                                                                                                                                                                              AA
  Score 67.5; Di
Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
               Ed. No. 3.3 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ESLLCPPSPKEVTCREMLTGGCLPWATRSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---VAPPGYQAYYCH----GEC-PFPLADHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; r12043; 3bMr.
InterPro; IPR002405; Inhibin_alpha.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00669; INHIBINA.
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q18657 PRELIMINARY; PI Q18657; Q18657; Q18657; Q1-NOV-1996 (TrEMBLrel. 01, Cre; 01-JAN-1998 (TrEMBLrel. 05, Las; 01-JUN-2002 (TrEMBLrel. 21, Las; C46C2.1 protein. C46C2.1. Caenorhabditis elegans. Eukaryota; Metazoa; Nematoda; C Rhabditidae; Peloderinae; Caeno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46929 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.7%; 25.3%;
  12.7%;
20.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                           Conservative
                                                                                                                                                                                                              PRELIMINARY;
                                                                                                              47 WIFWILLFSHHW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 23; Conser
               Local Similarity
nes 23; Conser
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7741;
                                                         m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
   Query Match
                                                                                                                                                                                                             Q9U418
Q9U418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                              Matches
                                                                                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
Q18657
                  Best
                                                                                                                                                                                               Q9U418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC DIT DIT OCC OCC OCC
                                                                                                                                                                                                                                                                                                                                                                                              RA RT RT CCC CCC DR DR DR DR DR DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qi
                                                                                                                                                                                                                                                                   DT DE GO OS OC OC OC OC OX RN RN RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ω
                                                                                                                                           g
                                                                                                                                                                                                                                        拮점
                                                                                     q
                                                                                                                 δ
```

ъ,

```
OX NCBL_TaxID=6239;
RP SEQUENCE FROM N.A.
RA MCMLTAY A.A.;
RA MCMLTAY A.A.;
R. Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases. RN [2]
RN [2]
RP SEQUENCE FROM N.A.
RA MODINE =99069613; PubMed=9851916;
RA MODINE =93069613; PubMed=9851916;
RA MODINE =93069613; PubMed=9851916;
RT investigating biology.",
RT investigating biology.",
RL Science 282:2012-2018(1998).
CC -1-SIMILARITY: BELLOWGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; Z68396; CASA9591.1; -CC -1-SIMILARITY: BELLOWGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR InterPro: IPRO0219; Ser_thr_pkinase.
DR FAME; PRO019; Ser_thr_pkinase.
DR PROMOF, PRO000001; Bub_pkinase.
DR PROMOF, PRO000001; Bub_pkinase.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS500108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS500118; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS500118; PROTEIN_
```

9, 2003, 15:06:30

Search completed: July Job time: 46.7788 secs

```
updates/sec
                                                                                                                                                                                        80. DAT: *
81. DAT: *
82. DAT: *
84. DAT: *
85. DAT: *
86. DAT: *
89. DAT: *
992. DAT: *
993. DAT: *
994. DAT: *
995. DAT: *
995. DAT: *
996. DAT: *
996. DAT: *
996. DAT: *
997. DAT: *
                                        Seconds
                                                                                                                                                                              Search time 8.92035 (Without alignments 239.005 Million cel.
                                                                                                                          908470
5.1.6
Compugen Ltd.
                                                                                                                        hits satisfying chosen parameters:
                                                                                                            133250620 residues
version
- 2003
                                                                                                                                                        0%
100%
45 summaries
                          model
                                        •-
                                      15:05:28
                                                                                               Gapext 0.5
                          MS
                                                                            1 FOANCGIDFIIFWIFW 16
GenCore
Copyright (c) 1993
                          using
                                                                                                                                     length: 0
length: 2000000000
                                                               US-09-854-133-587
98
                                                                                                                                                        Post-processing: Minimum Match
Maximum Match
Listing first
                                      2003,
                                                                                                           908470 segs,
                          - protein search,
                                                                                        BLOSUM62
Gapop 10.0
                                      δ
                                      July
                                                                                                                                                                                                                                                110
112
114
116
116
                                                                                                                                                                                        Total number of
                                                                                                                                     seq
                                                               Title:
Perfect score:
                                                                                        Scoring table:
                                                                                                                                     DB
DB
                          OM protein
                                                                                                           Searched:
                                                                            Sequence:
                                                                                                                                                                                  Database
                                                                                                                                     Minimum
                                                                                                                                           Maximum
                                      Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		Human T cell epito	Enzyme EPS11 invol	Amino acid sequech	Streptococcus pneu	Streptococcus pneu	CFE 95 protein sed	Human immune/haema	Human prostate can	Anti-CD4 antibody	Rat GPCR polypepti
SUMMARIES			ID		AAE13851	AAY54085	AAY43787	AAW99067	AAW99066	AAM01092	AAM84080	AAB57264	AAW54009	AAM51648
					22	21	21	20	20	22	22	21	19	23
			Length DB	, (16	504	504	207	326	326	20	64	123	285
	æ	Query	Match) { (((() 1	100.0	51.0	51.0			48.0	46.9	46.9	46.9	45.9
			Score) 	86	20	50	47	47	47	46	46	46	45
		Result	O		ᠳ.	7	m	4	2	9	7	æ	6	10

Human thoracic a Human thoracic a Human thoracic a Novel human G-pr Human G-pr Human G-protein	45 G protein coup 22 Human G-protei	Human membrane o RTA-like G prote	25 Drosophila me 30 Human polypep	75 Human polypept 12 Drosophila mel	30 Human thyroid st Humanised antibo	Human gene 43	92 Human	Human stomach c Human secreted	Human receptor	Human gene 43 e Human stromal c	79 Human s	Human polypepti	10 Hell	Helicobacter py	Human gene 50 en	Human albumin C6 himan eRv a	C6 human sFv ant	\sim	MENTS					tumour-specific protein.	<pre>imulant; cytostatic; gene therapy; esponse; lung cancer;</pre>							ecrist H, Benson DR, Indirias CY; , Elliot M, Mannion J, Kalos MD;
AAR4875 AAW0272 AAU7641	^1		~ ~	_ ~	_ ~	A 1/	•		^ .	•			•		AB8739			AAW0850 AAW0850	ALIGNMENT		AA.			to lung	mmunost mmune r							S PA
15 P 17 P 23 P 23 P	~ ~	CI CO C	20	0 0	o	. (2) (2)	י מ	0	⊢ (N (V)	~ -	1 m c	N O	~ ~	2 01	m m		m m			le; 16		2	ted	n; i e; i				.161)37.)37.)78. 7P.		Mohamath R, SP, Algate
298 298 323 327	343 343	(1) (1) (1299	151 1440	114	147	179	221 221	221	221	221 248	286	519	519	42	. 42	125	125 125			l; peptid		st entry	ope rela	ır protei 7, vaccin				.WO-US099	US-05380 US-05889 US-06408 US-23451 US-07045	RP.	J, ing
45.9 45.9 45.9 45.9	ы. М	ហេប	5.	44	. ო	mn	. n	m m	<u>.</u> د	ი ო .	m r		. m	د		9.0		0 0			ıdard		(fir	epit	tumou erapy pe.		12.		2001	2000 2000 2000 2000 2000	(A CO	les M Fl
11 12 45 13 45 45 45 45 45	5 45 6 45	7 45 8 45	450	4 4 4	3 4 43 3	5 43	7 43	8 4 3 9 4 3	43	443	3 4 4 4 3		7 43	8 0 43	4 4 2	1 42 42	3 4 .	4 5 42 7		LT 1 3851	AAE13851 stand	AAE13851;	26-FEB-2002	Human T cell	Human; lung t antisense-the T cell epitop	Homo sapiens.	WO200172295-A	04-OCT-2001.	28-MAR-2001;	29-MAR-2000; 05-JUN-2000; 18-AUG-2000; 22-SEP-2000; 01-NOV-2000; 14-DEC-2000;	(CORI-) CORIX	Reed SG, Lod Henderson RA,
																				SU E1	OI X	AC	DT	DE X	K K K K	SO	PN	PD	AA PF	R R R R R R S S	PA XX	PI

```
.;0
                                                                                                              The invention relates to isolated lung tumour-specific proteins and their corresponding cDNA molecules. Lung tumour-specific proteins and their antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer. The invention also relates to a composition useful for stimulating an immune response, and for treating cancer. The lung tumour specific oligonucleotide is useful in gene therapy and for diagnosis, detection and treatment of lung cancer. The present sequence is human T cell epitope related to lung tumour-specific protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        train LH59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exopolysaccharide; EPS; ESP enzyme; EPS1; EPS2; EPS3; EPS4; EPS5; EPS EPS7; EPS8; EPS9; EPS10; EPS11; Lactobacillus helveticus strain LH59; activated D-galactose pyranose; saccharide; beta-glycosyltransferase; undecaprenyl-phosphate-glycosyl-1-phosphate-transferase; alpha-glycosyltransferase; EPS polymerase; glycosyltransferase; phosphofuranose; transporter; food; fermented milk product; yoghurt; cheese; flavour stability; organoleptic property.
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of
                                            for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s,
ties
                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _{
m o}
                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exopolysaccharides
  improving propert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represent enzymes involved in the biosynthesis
                                          and polypeptides lung cancer -
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             involved in exopolysaccharide biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY54084; AAY54085
                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                           Score 98; DB 22;
Pred. No. 1.1e-08;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of e
for
                                       lung-specific polynucleotides and treatment of disease e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 8; Page 130-131; 162pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthesis
bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-097267/08.
N-PSDB; AAZ45259, AAY54082, AAY54083,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lamothe G
                                                                                      378pp; English
                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                               16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98EP-0201310.
98EP-0201311.
98EP-0201312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enzymes for
lactic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-EP02841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                  FQANCGIDFILFWIFW
                                                                                                                                                                                                                                                                                                                                                     FOANCGIDFILFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactobacillus helveticus
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Germond JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROD NESTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fermented milk products
              WPI; 2001-639201/73
                                                                                     378;
                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in
                                                                                        Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enzyme EPS11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9962316-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-APR-1998;
22-APR-1998;
22-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY54075-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stingele F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-DEC-1999
                                                                                                                                                                                                                                                                                                                     16;
                                          human
                                                           diagnosis
                                                                                                                                                                                                                                                                                           Ouery Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY54085;
                                                                                                                                                                                                                                                                                                                                                                                Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY54085
                                                                                     Claim 2;
                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                     \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NEST
                                                                                                                                                                                                                                                                                                                                                                                                                          AAY54085
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XX
KX
KX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PA
```

```
exopolysaccharides (EPS). These enzymes are designated EPS1-EPS11. and are encoded by open reading frames eps1-eps11. The enzymes are isolated from Lactobacillus helveticus strain LH59. The proteins are used in a method for the synthesis of EPS, which includes at least one step of forming a bond (alpha or beta-isomer) between C-1 (carrying the reducing aldehyde function, of an activated D-galactose pyranose), and a phosphate on a lipophilic or proteinaceous primer. Stepwise synthesis of EPS occurs with, in each step, addition of a new sugar unit, through its hemi-acetyl function, to an alcoholic hydroxyl of a second sugar unit, present at the end of a chain of sugar residues bonded to the primer. EPS1 has homology with an undecaprenyl-phosphate-glycosyl-1-phosphate-transferase; EPS2, EPS3 and EPS6 have homology with a beta-phosphate-transferase; EPS7 has homlogy with an EPS polymerase; EPS8 and EPS6 have homology with a beta-glycosyltransferase; EPS7 has homlogy with an EPS polymerase; EPS8 is a glycosyltransferase; EPS9 catalyses the transfer of phosphofuranose onto the following repetitive unit; EPS10 transferot of formed or not the EPS111 is involved in the synthesis and export of formed polysaccharides. The EPS enzyme are used to improve properties of foods, particularly fermented milk products such as yoghurt and cheese, e.g. their organoleptic properties and flavour stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of exopolysaccharides having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   properties or useful in fermented milk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the eps11 of Lactobacillus helveticus LH59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eps operon; Lactobacillus helveticus LH59; enzyme; eps1; eps2; eps3; eps4; eps5; eps6; eps7; eps8; eps9; eps10; eps11; exopolysaccharide biosynthesis; EPS; intersugar bond; antitumour; probiotic; foodstuff; organoleptic quality; flavour; lactic acid bacteria; acidified milk product; yoghurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY43784, AAY43785, AAY43786, AAY43787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5,
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50; DB 21;
Pred. No. 8.6;
; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 8; Page 131-132; 163pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lamothe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98EP-0201310.
98EP-0201311.
98EP-0201312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-EP03011.
                                                                                                                                                                                                                                                                                                                                                                                                                          51.0%;
larity 37.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or probiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YRSKCIVTFMHFWFFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FQANCGIDFIIFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     helveticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Germond JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROD NESTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequecne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-013255/01
N-PSDB; AAZ30356, A
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
6; Conser
                                                                                                                                                                                                                                                                                                                                                                                           504 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antitumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lactobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-APR-1998;
22-APR-1998;
22-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09954475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         soc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY43787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY43787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stingele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NEST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY43787
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PR
PR
PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DR DR XX XX PT PT
```

ô

δ

В

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents the ORF protein sequence of an isolated Phospho-N-acetylmuramoyl-pentapeptide-transferase designated mray. Mray polynucleotides and proteins are useful for diagnosing susceptibility to diseases by detecting mutations or polymorphisms in the mray gene or analysing for the presence of amount of mray protein expressed in a
             Lactobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     otitis media;
endocarditis;
                       helveticus LH59. The operon contains 11 open reading frames, and encodes enzymes (eps1. eps2, eps3, eps4, eps5, eps6, eps7, eps8, eps9 and eps11) that are involved in the biosynthesis of exopolysaccharides (EPS). The enzymes catalyse the formation of specific intersugar bonds. The enzymes catalyse a process that includes at least one step of forming a bond (in alpha or beta anomeric form) between C1, carrying the reducing aldehyde group of an activated D-Galp (galactose in pyranose form), and a phosphate group on a lipophilic or proteinaceous primer. The enzymes are used to produce EPS that have antitumor or probiotic properties or are used in foodstuffs to improve organoleptic qualities and flavour. When expressed by lactic acid bacteria, EPS impart a free-flowing character and/or a smooth, creamy texture to acidified milk products (yoghurt or cheese).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neumonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Phospho-N-acetylmuramoyl-pentapeptide-transferase (mraY) polypeptide and polynucleotide - useful as diagnostic reagents for prevention and treatment of Streptococcus pneumoniae infections, which cause otitis media and meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nence
encoded by the eps operations 11 open reading frames,
                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae, mraY, transferase, infection; pl
phospho-N-acetylmuramoyl-pentapeptide-transferase family;
bacteraemia; conjunctivitis; sinusitis; pleural empyema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transferase ORF protein seq
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lonetto MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                    Score 50; DB 2
Pred. No. 8.6;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kosmatka AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; Protein; 207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BEECHAM PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae mraY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129
               enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0061156.
97US-0055467.
                                                                                                                                                                                                                                                                                                                                                                                    51.0%;
37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98EP-0304635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BEECHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FOANCGIDFIIFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YRSKCIVTEMHEWFFW
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jaworski DD,
          helveticus LH59. The c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1999-134240/12
)B; AAX18943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMITHKLINE
SMITHKLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang M;
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                           504 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-1998;
12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP897007-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                meningitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JL,
CM,
                                                                                                                                                                                                                                                                                                                                                                                                                              .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW99067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW99067
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fueyo J
Traini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK
(SMIK
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                            Best
```

XX

XXX

XX PF XX PR PR PR PA PA

XX PI PI XX

DR DR

XX PT PT PT

```
patient sample. Mray PCR probes are useful for diagnosing diseases, and can characterise the response of the infectious organism to drugs. Mray proteins and polynucleotides are also useful for screening for antagonists, agonists and drugs against infectious micro-organisms. Mray agonists and antagonists are bacteriostatic and bacteriocidal compounds which can be used in treatment to enhance (agonist) or block (antagonist or antisense sequence) mray activity, therefore treating microbial diseases, especially Streptococcus pneumoniae diseases including otitis media, bacteraemia, conjunctivitis, pneumonia, sinusitis, pleural empyema, endocarditis and especially meningitis. Epitopes of mray proteins and polynucleotides are useful immunogens (vaccines) for producing anti-mray antibodies for prevention of bacterial infections, and mray polynucleotides can be used in genetic immunisation (gene therapy) to prevent infections. Mray proteins, polynucleotides and their (ant)agonists can prevent adhesion of bacteria to matrix proteins, and are useful for use on wounds and body implants to prevent bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae; mraY; transferase; infection; pneumonia; phospho-N-acetylmuramoyl-pentapeptide-transferase family; otitis media; bacteraemia; conjunctivitis; sinusitis; pleural empyema; endocarditis; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents an isolated Phospho-N-acetylmuramoyl-pentapeptide-transferase designated mraY. MraY polynucleotides and
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reagents and
                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Phospho-N-acetylmuramoyl-pentapeptide-transferase (mraY) polypeptide and polynucleotide - useful as diagnostic reagen for prevention and treatment of Streptococcus pneumoniae infections, which cause otitis media and meningitis
                                                                                                                                                                                                                                                                                                                                           Length 207;
                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lonetto MA;
                                                                                                                                                                                                                                                                                                                                                                            ₹;
                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae mraY transferase.
                                                                                                                                                                                                                                                                                                                                          Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kosmatka AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 4; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM COR (SMIK ) SMITHKLINE BEECHAM PLC
                                                                                                                                                                                                                                                                                                                                         48.0%;
ilarity 43.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             16
                                                                                                                                                                                                                                                                                                                                                                                                                               :| : || :|| :|| 24 YQVHLGIFYIVFALFW 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0061156
97US-0055467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98EP-0304635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               FOANCGIDFIIFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jaworski DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-134240/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang M;
                                                                                                                                                                                                                                                                                                                                                       Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                         207 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAX18942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-APR-1998;
12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP897007-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fueyo JL,
Traini CM,
                                                                                                                                                                                                                                                                         infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW99066;
                                                                                                                                                                                                                                                                                                                                                                                                               <del>--1</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW99066
                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW99066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
      Dp
                                                                                                                                                                                                                                                                                                                                                                                                               δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CI
```

```
proteins are useful for diagnosing susceptibility to diseases by detecting mutations or polymorphisms in the mray gene or analysing for the presence of amount of mray protein expressed in a patient sample.

Mray PCR probes are useful for diagnosing diseases, and can characterise the response of the infectious organism to drugs. Mray proteins and polymucleotides are also useful for screening for antagonists, agonists and antagonists are bacteriostatic and bacteriocidal compounds which can be used in treatment to enhance (agonist) or block (antagonist or antisense sequence) mray activity, therefore treating microbial diseases, especially Streptococcus pneumoniae diseases including otitis media, bacteraemia, conjunctivitis, pneumonia, sinusitis, pleural empyema, endocarditis and especially meningitis. Epitopes of mray proteins and polynucleotides are useful immunogens (vaccines) for producing anti-mray antibodies for prevention of bacterial infections, and mray proteins, may proteins. Mray proteins, polynucleotides and their (antibodists can prevent adhesion of bacterial to matrix proteins, and are useful for use on wounds and body implants to prevent bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                l empyema,
proteins and
cing anti-mray
                                                            can characterise
                                                                                                                             which can be cor antisense
                                                                                              sts, agonists
s and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bacterial antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to nucleic acids (AAH90701-AAH90918) encoding polypeptides (AAM01002-AAM01114), which are essential for the viability of a bacterial cell wall. The acronym CFE stands for "CEG For
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               viability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bruccoleri RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ч
                                                                                                                                                                                                                                                                                                                                                                                                Length 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes involved the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibacterial; vaccine; gene therapy; bacterial cell wal CFE; CEG; Conserved Essential Gene; bacterial infection; antisense therapy; antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Davison DB,
                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                DB 20;
                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB
Pred. No. 17;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 targets for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding conserved essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; Pages 342-343; 380pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dougherty BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein; 326 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e potential infections -
                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BRIM ) BRISTOL-MYERS SQUIBB
                                                                                                                                                                                                                                                                                                                                                                                            48.0%;
larity 43.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0174089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-US35604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FOANCGIDFIIFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replication which are resistant bacterial in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pucci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-496721/54.
N-PSDB; AAH90791.
                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                            326 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200149721-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dougherty
Thanassi J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM01092;
                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM01092
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
          8×8666666666666666666668888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DR
DR
XX
```

```
Expression", where CEG stands for "Conserved Essential Gene". The nucleic acids are useful for detecting the presence of proteins essential for the viability of a bacterial cell wall in samples such as cells, tissues, biological fluids, blood, serum, nose, ear or throat swabs with ligands, and for detecting corresponding target nucleic acid molecules with complementary sequences. The nucleic acids are also useful for determining whether a genomic nucleotide sequence of interest is essential for viability of a bacterial cell or whether it resides within an open reading frame of the genomic sequence of interest comprising 200-500 base pairs) into the genomic sequence of interest comprising 200-500 base pairs) into the genomic sequence of interest which confers a selection agent such as chloramphenicol. The nucleic acids and proteins are also useful as vaccines and for treating bacterial infections with gene therapy and antisense therapy. The nucleic acids also enable identification of targets suitable for the treatment of antibiotic resistant bacterial infections.
                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune; haematopoietic; immune/haematopoietic antigen; cancer; tic; gene therapy; vaccine; metastasis.
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                        Length 326;
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:11673.
                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                              Score 47; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                     .
,
                                                                                                                                                                                                                                                                                                                                                                                   :| : || :|:| || XQVHLGIFYIVFALFW 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0179065.

2000US-0180628.

2000US-0184664.

2000US-0186350.

2000US-0190076.

2000US-0198123.

2000US-0209467.

2000US-0209467.

2000US-0214886.

2000US-0214886.

2000US-0214886.

2000US-0214886.

2000US-0214880.

2000US-0215135.

2000US-0216847.

2000US-0216880.

2000US-0225213.

2000US-0225213.
                                                                                                                                                                                                                                                                                                                                                                   1 FOANCGIDFIIFWIFW 16
                                                                                                                                                                                                                                                                                                        48.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM84080 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune/haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001WO-US01354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 7; Conser
                                                                                                                                                                                                                                                                           326 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-2000
14-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM84080;
                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
   $$$$$$$$$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XX
```

```
20000US - 02252670.
20000US - 02252670.
20000US - 0225270.
20000US - 02252770.
20000US - 02257577.
20000US - 02257577.
20000US - 02257577.
20000US - 0225758.
20000US - 0225759.
20000US - 02234997.
20000US - 0234997.
20000US - 02346474.
20000US - 02446477.
20000US - 0246477.
14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

15-SEP-2000;

16-SEP-2000;

17-SEP-2000;

17-SEP-2000;

18-AUG-2000;

18-AUG-2000;

19-SEP-2000;

10-SEP-2000;

11-SEP-2000;

11
```

```
2000US-0246526.
2000US-0246528.
2000US-0246532.
2000US-02466532.
2000US-0246610.
2000US-0246611.
2000US-0249207.
2000US-0249209.
2000US-0249211.
2000US-0249211.
2000US-0249212.
2000US-0249213.
2000US-0249214.
2000US-0249218.
2000US-0249218.
2000US-0249218.
2000US-0249218.
2000US-0249218.
2000US-0249218.
2000US-0249219.
2000US-0249218.
2000US-0251988.
2000US-0251868.
2000US-0251869.
2000US-0251869.
2000US-0251869.
2000US-0251869.
2000US-0251869.
08-NOV-2000;

08-NOV-2000;

08-NOV-2000;

08-NOV-2000;

08-NOV-2000;

08-NOV-2000;

17-NOV-2000;

17-NOV-2000;
                                                                                                                                                                                                                              01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                      08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
                                                                                                                                                                                                                                                                                                                 11-DEC-2000;
05-JAN-2001;
```

(HUMA-) HUMAN GENOME SCI INC.

SM; Ruben Barash SC, Rosen CA,

01-483426/52. AAK56861. 2001 N-PSDB; WPI;

acids encoding human immune/hematopoietic antigen polypeptides, or preventing, diagnosing and/or treating cancers and for preventing, metastasis Nucleic useful

+ Sequence Listing; English 11673; 3071pp Claim 11; SEQ ID NO

amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic antino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic actived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK84950 and AAM82169 crepresent sequences used in the exemplification of the present invention.

9

Wed

q

δ

ns

40

::|||:||:|: ESNCGLDFVSFF

```
gynaecological;
renal;
                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostic
d to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the present
                                                                                                                                                                                                                                                                                                                                                                                     diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or research purposes. The prostate cancer antigens may be used to treadisorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the presen
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as prostate
diagnosis of
                                           ÷
                                                                                                                                                                                                                                                                                                                                            cancer antigen protein sequence SEQ ID NO:1842
                                                                                                                                                                                                                                                                                                                                                                                                  cardicactive; immunomodulatory nephrotropic; antiinfective; gneural; immune; reproductive; cardiovascular; proliferative
                                                                                                                                                                                                                                                                                                                                                                                 cancer antigen; detection
      Length 50;
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer associated gene sequences, referred to
   22;
  ore 46; DB 2 ed. No. 4.1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
   Score
Pred.
                                                                                                                                                                                                                      AAB57264 standard; Protein; 64 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders such as prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                Human; prostate cancer; prostate neuroprotective; cytostatic; card vulnerary; gastrointestinal; nephantibacterial; gene therapy; neur gastrointestinal; pulmonary; card wound; infectious disease.
                                          4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2338pp;
46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000WO-US05988
                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                16
                                           Conservative
                                                                                 NCGIDFILFWIFW
                                                                                                                     NCCYOFLIFFLYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-587513/55
B; AAF16467.
                      Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antigens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page
                                                                                                                                                                                                                                                                                                                                           prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200055174-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ROSE/) ROSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-1999;
                                                                                                                                                                                                                                                                                                    13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA,
                                                                                                                                                                                                                                                             AAB57264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11;
                                                                                4
                                                                                                                      12
  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer
                                                                                                                                                                                                                                                                                                                                            Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen
                                        Matches
                                                                                                                                                                              RESULT
AAB5726
```

XXX

ΚX

XX OS XX PN

XX XX XX XX XX XX XX

PA XX PI

PA

```
This sequence represents the VH5 domain of an anti-CD4 antibody

(Ab). This sequence can be used in the method of the invention for

treating a subject, where the treatment comprises administration of an

Ab. The method comprises the administration of an antibody which has an

old World monkey (e.g. baboon or macaque) variable region which binds to

method is useful for the treatment of eczema and immuno-modulated

diseases and especially rheumatoid arthritis. The recombinant antibodies

cused are sufficiently different from native monkey antibodies to allow

human antigens to raise these antibodies, but similar enough to human

compared to antibodies used in therapy in prior art, these antibodies do

not induce human anti-antibodies on repeated administration. They also

have longer half-lives and do not have a lack of effector function with
                                                                                                                                           variable heavy domain;
immuno-modulated disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n antibody constant do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46; DB 1
Pred. No. 9.5;
0; Mismatches
                                                                                                                                           human; therapy;
domain; eczema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              variable region and
                                                                                                                5-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Improved method for antibody treatment an Old World monkey variable region and
                                                                                                                clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84pp; English
                           123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                       RW
                                                                                                                                                                                                                                                                                                                   92US-0912292.
91US-0735064.
92US-0856281.
95US-0379072.
                                                                                                               antibody VH5 monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.9%;
ilarity 58.3%;
Conservative
                           Protein;
                                                                                                                                                                                                                                                                                         95US-0476349
                                                                                                                                                                                                                                                                                                                                                                                                                                       Raab
                                                                                                                                         Anti-CD4 antibody; monkey;
Old World monkey; constant
rheumatoid arthritis.
                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGIDFIIFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36
                                                                                                                                                                                                                                                                                                                                                                                                             PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGFSFTGFWISW
                                                                                                                                                                                                                                                                                                                                                                                                                                       Newman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-296690/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9e;
                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig
                                                                                                                                                                                                                                                                                                                   10-JUL-1992;
25-JUL-1991;
23-MAR-1992;
05-DEC-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                          (IDEC-) IDEC
                                                                                                                                                                                                                                                                                         07-JUN-1995;
                                                                                  29-JUL-1998
                                                                                                                                                                                                     Primate sp.
                                                                                                                                                                                                                                US5750105-A
                                                                                                                                                                                                                                                            12-MAY-1998
                                                      AAW54009;
                         AAW54009
                                                                                                               Anti-CD4
                                                                                                                                                                                                                                                                                                                                                                                                                                       ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
          AAW54009
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best
                                                                                                              XX
OS
XX
PN
XX
                                                                                                                                                                                                                                                          YXX
YXX
YXX
YXX
PR
PR
PR
PR
                                                                                                                                                                                                                                                                                                                                                                                           XX
XX
XX
XX
XX
DR
PT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

ö

AAM51648 standard; Protein; 285 AA.

RESULT 10 AAM51648 ID AAM51

ö

Gaps

ö

Indels

1;

Score 46; DB 21; Pred. No. 5.1; ; Mismatches

5;

46.9%; larity 50.0%; Conservative

Similarity 6; Conser

Query Match

Best Local Matches

QANCGIDFILFW 13

0

Length 64;

Wed

```
09-SEP-1993;
10-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5508384-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-SEP-1992;
                                                                                                                                                                          Polypeptides
binding GPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-APR-1996.
WO9405695-A1
                                                  09-SEP-1993;
                                                                         10-SEP-1992;
                        17-MAR-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murphy RB,
                                                                                                                         RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW02727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW02727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                         Murphy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW02727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XX
DT
DE
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G-protein coupled receptor; ligand binding assay; transmembrane domain; psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin; muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine; rhodopsin; opsin; odorant; cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for treating a disease or condition mediated by human proteases. The present sequence is a rat GPCR polypeptide used in comparison studies with the polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the sequence
GPCR
                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated human G protein-coupled receptor (GPCR) polypeptide that is related to the MAS proto-oncogene receptor subfamily. The polypeptide comprises a fully defined sequence of 289 amino acids as given in the specification, or its fragment comprising 10 contiguous amino acids, or an amino acid sequence of an allelic variant or orthologue of the amino acid sequence given in the sequence polypeptide is useful for identifying a modulator of a GPCR useful for treating a disease or condition it. The polypeptide is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                            related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                           t is
and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human thoracic aorta G-protein coupled receptor protein.
                                                                                                                                                                                                                                                                                                                                          Novel human G protein-coupled receptor polypeptide that MAS proto-oncogene receptor subfamily, useful as model developing human therapeutic agent -
                                                                                       Rat; G-protein coupled receptor; GPCR; gene therapy; MAS proto-oncogene receptor; human protease; disease.
                                                                                                                                                                                                                                                                                          Beasley EM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB Pred. No. 30; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                          Di Francesco V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 AA.
                                                                                                                                                                                                                                                                                                                                                                                              2; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein;
                                                                                                                                                                                                                            24-APR-2000; 2000US-199149P 04-AUG-2000; 2000US-0633146
                                                                                                                                                                                                     2001WO-US13097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
                                                                 GPCR polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIDFILFWIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||: :||:|
GIDWFLFWVF
                                                                                                                                                                                                                                                                                                                    2002-049265/06
                                                                                                                                                                                                                                                                                          Cravchik A,
                                                                                                                                                                                                                                                                  (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 AA;
                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig
                                                                                                                                                      WO200181409-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens.
                                                                                                                                                                                                     24-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1996
                                        20-FEB-2002
                                                                                                                                                                               01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                               ^{\mathrm{d}s}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR48755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR48755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                              Rattus
                                                                                                                                                                                                                                                                                            Wei M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                 Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
```

δ

```
proteins AAR48685-R48758 represent a range of G-protein coupled receptor proteins selected from cAMP, adenosine, muscarinic acetylcholine, adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin, odorant, cytomegaloviral and other G-protein coupled receptors. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G-protein coupled receptor; ligand binding assay; transmembrane domain; schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin; muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin; odorant; cytomegalovirus; serotonergic.
                                                                                                                                                                                                                                                                   - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                   tides of G-coupled receptor proteins (GPRs) GPR ligands or modulating GPR binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G-protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 AA
                                                                                                                                                                                                                                                                                                                                                  130-131; 160pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92US-0943236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-0118270.
92US-0943236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.9%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; peptide;
93WO-US08528
                                                      92US-0943236
                                                                                                            (UYNY ) UNIV NEW YORK STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schuster DI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
6; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thoracic aorta
                                                                                                                                                                   Schuster
                                                                                                                                                                                                                    WPI; 1994-101120/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIDWFLFWVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIDFILFWIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 AA;
                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page
```

```
Proteins AAW02657-W02730 represent a range of G-protein coupled receptor (GPR) proteins selected from CAMP, adenosine, muscarinic acetylcholine, adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin, odorant, cytomegaloviral and other GPR proteins. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see AAW02747-W02999 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e; dementia;
re; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rder; COD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n; asthma;
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iarrhoea;
                                        e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-protein coupled; receptor; IGPCR18; cardiovascular system disors signal processing; female reproductive tissue; infertility; cardiovascular disease; coronary heart disease; heart attack; strainflammatory disorder; metabolic disorder; uterus; placenta; ovar prostate; reproductive disorder; pain; cancer; CNS disorder; central nervous system disorder; schizophrenia; episodic paroxysmal anxiety; EPA; obsessive compulsive disorder; demy huntingdon's disease; multiple sclerosis; Alzheimer's disease; demy Huntingdon's disease; anorexia; kidney disease; renal failure; obj gastrointestinal disorder; irritable bowel syndrome; IBS; diarrhownotility disorder; gastric emptying; osteoporosis; infection; ast allergy; arthritis; sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                     agent,
                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        r protein, IGPcR18, useful
or treatment of pain, cand
                                                                                                                                                                                                                                                                                                                                             Length 298;
                                    antipsychotic
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human G-protein coupled receptor IGPCR18.
                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nehls MC;
                                                                         Column 173-176; 184pp; English
                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                          ed. No. 31;
Mismatches
                                    as
                                 useful
                                                                                                                                                                                                                                                                                                                                          Score 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-coupled receptor prevention, amelioration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein; 323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trommler P,
                                                                                                                                                                                                                                                                                                                                                          Pred
                                                                                                                                                                                                                                                                                                                                                                      3;
                                peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001WO-EP07530.
                                                                                                                                                                                                                                                                                                                                                         larity 60.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                          45.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000; 2000US-215879P
                                               schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AG
                                                                                                                                                                                                                                                                                                                                                                                                                                   220
                                                                                                                                                                                                                                                                                                                                                                                                     15
                                receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INGE-) INGENIUM PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             တွ
1996-208785/21
                                                                                                                                                                                                                                                                                                                                                                                                     GIDFIIFWIF
                                                                                                                                                                                                                                                                                                                                                                                                                               GIDWFLFWVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wattler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002-140079/18
                                                                                                                                                                                                                                                                                                                                                       Similarity 6; Conser
                                                                                                                                                                                                                                                                                                           298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK15133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200202598-A2.
                              dopamine
                                                treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens.
                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [되
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU76411;
                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                  211
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU76411
                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wattler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ношо
                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU76411
                                          ă
                                                                                                                                                                                                                                                                                                                                                                                                                               α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XX
XX
XX
XX
PA
XX
XX
```

; 0

```
protein, IGPCR18 (1). (1), the polynuclectide (II), agonists and antagonists of (1)/(II) are useful for the diagnosis and treatment of cardiovascular system disorders, the detection of mutant or inappropriately expressed forms of IGPCR18, and for drug screening. (I) is useful in treatment of diseases associated with signal processing in female reproductive tissues, such as infertility, cardiovascular diseases such as coronary heart disease, heart attack and stroke, inflammatory disorders and metabolic disorders linked to reproductive tissues like uterus, placenta, ovary and prostate, reproductive disorders, pain, cancer, central nervous system disorders such as schizophrenia, episodic paroxysmal anxiety (EPA) disorders such as schizophrenia, episodic paroxysmal anxiety (EPA) disorders such as schizophrenia, disorder (ICDD), Parkinson's disease, moltility disorders such as renal failure, obesity, gastrointestinal cisorders such as tritable bowel syndrome (IBS), diarrhoea, motility disorders such as bacterial, fungal, protozoal and viral infections, asthma, allergy, arthritis, and sepsis. (I) is useful for the products involved in regulating IGPCR18, and as pharmaceutical reagents. (II) is useful for mapping the location of the gene to the chromosome, and to detect abnormalities involving IGPCR18 gene structure. This is the amino acid sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virus; HIV; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGS43; G-protein coupled receptor; GPCR; uterus; lung; trachea; colon; small intestine; stomach; mammary gland; prostate; testis; psychiatric disorder; central nervous system disorder; schizophrenia; episodic and paroxysmal anxiety disorder; Parkinson's disease; multiple sclerosis; Alzheimer's disease; cardiovascular disease; heart failure; angina pectoris; kidney disease; dyslipidaemias; obesity; emesis; gastrointestinal disorder; inflammatory bowel disease; diabetes; osteoporosis; inflammation; infection; human immunodeficiency virus; HIV cancer; immune disorder; urinary retention; asthma; allergy; arthritis; benign prostatic hypertrophy; endotoxin shock; sepsis; gene therapy; gynaecological disorder; vaccine; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                            ed receptor
agonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 323;
      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                            -conbled
  metabolic, reproductive, gynaecological,
  disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ed. No. 34;
Mismatches
                                                                                            Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G-protein coupled receptor, IGS43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45;
Pred. No.
                                                                                           novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE14729 standard; Protein; 327 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                     2; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.98;
60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001WO-EP11319
                                                                                              Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                         describes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIDFILFWIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIDWFLFWVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 AA;
inflammatory, n
cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200228897-A2.
                                                                                        The invention
                                                      Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                    8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE14729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238
                                                    \mathtt{Claim}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XX
```

2000EP-0203411.

02-OCT-2000;

incer,

diagnosis,

Φ

```
peripheral vascular disease, Raymand's disease, kidney disease, dyslipidaemias, obesity, emesis, gastrointestinal disorders including irritable bowel syndrome, inflammatory bowel disease, diabetic gastroparesis and diabetes, ulcers, diarrhoea, osteoporosis, inflammations, infections including bacterial, fungal, protozoan and viral infections, pain, cancers, chemotherapy induced injury, tumour invasion, immune disorders, urinary retention, asthma, allergies, arthritis, benign prostatic hypertrophy, endotoxin shock, sepsis, complications of diabetes mellitus, and gynaecological disorders. The polypeptide and polynucleotide of the invention are also useful so research reagents and materials for discovery of treatments and diagnostics to animal and human diseases. The polypeptide is also useful for chromosome identification. The polypeptide is also useful for assessing the binding of small molecule substrates and ligands in cells, cell-free preparations, chemical libraries and natural product mixtures. The present sequence is human IGS43 GPCR.
                                                                                                                                                                                                                                                                                                                                                             The invention relates to IGS43 G-protein coupled receptor (GPCR) and the polynucleotide encoding it. The IGS43 polypeptide, polynucleotide, egonist, antagonist or antibody is useful for treating dysfunctions or disorders related to uterus, kidney, lung, trachea, colon, small intestine, stomach, mammary gland, prostate, testis, central nervous cystem, cerebellum and spinal cord. The polypeptide is useful as vacine for inducing immunological response in a mammal, for treating cysthiatric and central nervous system disorders including conjulsive disorder, post traumatic disorder, phobia and panic, major depressive disorder, bipolar disorder, parkinson's disease, general anxiety disorder, autism, delirium, multiple sclerosis, Alzheimer's disease, dementia, severe mental retardation, Huntington's disease, disease, dementia, stroke, addiction/dependency/craving, sleep canciovascular diseases including heart failure, angina pectoris, arrhythmias, myocardial infarction, cardiac hypertrophy, hypotension, hypertension, thrombosis, arteriosclerosis, cerebral infarction, cardiac hypertrophy, hypotension, constructs and including permandial including correbral infarction, cardiac hypertrophy, hypotension, hypertension, thrombosis, arteriosclerosis, cerebral infarction, cardiac hypertrophy, disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eful as vaccine
                                                                                                                                                                                                                                                                                                                                                                        and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         obsessive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vity disorder
                                                                                                                                                                                                                      and nucleic
                                                                                                                                                                                                                                            of uterus
                                                                                                                                                                                                                                                                                                                                                                                                                       sfunctions or
                                                                                                                                                                                                                                                                      testis
                                                                                                                                                                                                                                                  ers
                                                                                                                                                                                                                   l G-protein coupled receptor, termed IGS43 polypeptide encoding the polypeptide, useful for treating disordery, lung, colon, stomach, mammary gland, prostate and
                                                                                                 De Moor L;
                                                                                                                                                                                                                                                                                                                           English.
2000US-237394P
                                                                                                 Blockx H,
                                                (SOLV ) SOLVAY PHARM BV
                                                                                                                                                                                                                                                                                                                             29pp;
                                                                                                                                           WPI; 2002-426102/45.
N-PSDB; AAD31159.
                                                                                                                                                                                                                                                                                                                        7;
                                                                                                 Deleersnijder W,
                                                                                                                                                                                                                                                                                                                            Claim 25; Page
                                                                                                                                                                                                                                                                             kidney, lung,
 04-OCT-2000;
                                                                                                                                                                                                                              Novel
```

```
ö
                             Gaps
                             ö
             7;
              Length 32
                              Indels
                             1;
              23;
            Score 45; DB
Pred. No. 34;
3; Mismatches
              DB
              45.9%;
larity 60.0%;
Conservative
                                              15
                                              6 GIDFILFWIF
                      Similarity 6; Conser
327 AA;
Sequence
              Query Match
Best Local
                        Best Loc
Matches
```

249

240 GIDWFLFWVF

d

ŏ

ö

2003, 15:07:41

6

July

secs

Search completed: Job time: 9.92035

265

|||::||:| 256 GIDWFLFWVF

ga

ŏ

15

6 GIDFIIFWIF

```
RESULT 15
AAR96145
ID AAR96145 standard; Protein; 343 AA.
XX
AC AAR96145;
XX
DT 29-OCT-1996 (first entry)
XX
DE G protein coupled receptor protein.
```

```
G protein coupled receptor (GCR) proteins can be used to identify ligands which act as antagonists of GCR/ligand binding. Such ligands can be used for promoting or inhibiting physiological responses such as liberation of arachidonic acid, acetylcholine and endocellular calcium, endocellular cyclic AMP production, production of inositol, changes in cell membrane potential, phosphorylation of endocellular proteins, activation of c-fos, lowering of pH, activation of G protein and cell promulgation. The GCR products can also be used for the detection of ligands and in the production of antibodies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
G protein coupled receptor protein; GCR; identification; detection; ligands; physiological response; arachidonic acid; acetylcholine; calcium; cyclic adenosine monophosphate; cAMP; inositol; membrane potential; phosphorylation; c-fos; antibodies; transgenic animals.
                                                                                                                                                                                                                                                                                                                                               t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                           New isolated rabbit G protein receptor protein - used partic. identify agonists or antagonists which can promote or inhibit physiological responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 30-32; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                              Kawamata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.9%;
60.0%;
                                                                                                                                                                                                                                                TAKEDA CHEM IND LTD.
                                                                                                                                                                              95EP-0117786
                                                                                                                                                                                                        95JP-0215798
94JP-0279545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                             Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                       1996-232096/24
)B; AAT27218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transgenic animals
                                                                                                                                                                                                                                                                             Hinuma S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343 AA;
                                                                                                                                                                                                        24-AUG-1995;
14-NOV-1994;
                                                                                                                                                    15-MAY-1996.
                                                                                                                                                                               11-NOV-1995;
                                                                                                                        EP711831-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                    (TAKE)
                                                                                                                                                                                                                                                                             Fuji R,
                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
```

	·			
			•	
·				
	·			
		-		
				•

```
updates/sec
                                                            Search time 4.95575 Seconds (without alignments) 94.994 Million cell updates
                                                                                                                                                                                                262574
5.1.6
Compugen Ltd.
                                                                                                                                                                                                hits satisfying chosen parameters:
                                                                                                                                                                           262574 seqs, 29422922 residues
 version
- 2003
                                          using sw model
                                                             2003, 15:05:28
                                                                                                                                                       0.5
 GenCore
(c) 1993
                                                                                                                         ٦
                                                                                                                                                        Gapext
                                                                                                                         FQANCGIDFITFWIFW
                                                                                                                                                                                                                    length: 0
length: 2000000000
                                                                                                 US-09-854-133-587
98
                                                                                                                                             BLOSUM62
Gapop 10.0 ,
                                         protein search,
           Copyright
                                                             6
                                                           July
                                                                                                                                                                                                of
                                                                                                                                                                                                                    sed
                                                                                                               Perfect score:
                                                                                                                                              Scoring table:
                                                                                                                                                                                                Total number
                                                                                                                                                                                                                    DB
DB
                                          OM protein
                                                                                                                         Sequence:
                                                                                                                                                                            Searched:
                                                                                                                                                                                                                    Minimum
                                                                                                                                                                                                                                Maximum
                                                              ou:
                                                                                                     Title:
                                                              Run
```

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/fB_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		dФ			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
	4	46.	12	-		quence 82, App
7		٠.	$^{\circ}$	1	76-34	e 82, App
e		ص	σ	-	-118-270-7	76, App
4		ر. د	9	വ	528-	76, App
വ		2	$^{\circ}$	7	-665-20	equence 45
9		₹.	$^{\circ}$	7	-202-4	46
7		∵	7	7	-665-202-4	49
80		₹.	\sim	7	65-202-5	51
6		4	4	~	-483-151-	7
10		7	Н	4	-134-00	40
11		ij	Н	~	18-15	2
12		_;		7	-318-157B-1	12
13	41	41.8	119	~	US-08-318-157B-17	
14		ij.	$^{\circ}$	7	-665-202-4	48
15		ij	7	7	-08-665-202-5	50
16		÷	$^{\circ}$	7	-665-202-5	52
17		÷	~	~	-08-665-202-	53
18		ij	$^{\circ}$	~	-08-665-202-5	54
19		귿	7	7	-08-665-202-5	55
20		ij.	\sim	7	-08-665-202-	57
21		\vdots	3	7	6 - 31	7
22		.	3	7	-09-136-315-	9
23		0	┰┥	7	-318-157B-	8
24		。		7	-08-318-1	6
25		0	⊣	7	-31	10
26		0	119	7	-08-318-157B-1	11
27		。	119	7	US-08-318-157B-13	13

, App	, App	O.	, App	_	Sequence 4, Appli	$\overline{}$	Appl	Q,	3, App	_	2, Appl	4, App	a	, App	_	Seguence 5, Appli	Sequence 3, Appli
-157	B-1	US-09-124-141-13	-141-2	41-	US-08-592-696-4	7-5	US-09-028-148-4	-124-	4-141-	-242-689-	US-08-468-583-2	1-8	US-08-576-626A-44	3-74	US-08-480-882B-5	US-08-480-210-5	US-08-220-401-3
7	~	4	4	4	~	7	m	4	4	٦	4	က	~	က	٦	Н	П
	$\overline{}$	\circ	\circ	σ	594	$^{\circ}$	$\boldsymbol{\sigma}$	O	σ	\sim	\sim	9	36	М	9	262	9
	0				40.8	0	0			0		0	6	9	σ	δ	
40	40	40	40	40	40	40	40	40	40	40	40	39.5	39	39	39	39	39
					33												

ALIGNMENTS

```
RESULT 1

19-08-478-039-82

19-08-478-039-82

Sequence 82, Application US/08478039

Patent No. 5681722

CENERAL INFORMATION:

APPLICANT: Hanna, Nabil

APPLICANT: Hanna, Nabil

APPLICANT: Rabb, Ronald W.

TITLE OF INVERTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114

APPLICANT: Alexandria

STREET: 699 PRINCS SL.

CITY: Alexandria

STREET: 699 PRINCS SL.

CITY: Alexandria

STREET: 100 PRINCS SL.

CONFIRK: 100 ARCOMPANIE ROMABLE FORM:

COMPUTER: THE PCOMPATION ACCOMPANIES.

SOFTWARE: Patentin Release #1.0, Version #1.30

CURSSITION NUMBER: US/08/478,039

FILING DATE: 07-UN-1995

RIGHEN APPLICATION DATA:

APPLICATION NUMBER: US 07/912,292

FILING DATE: 10-UL-1991

RECOMPANIE: 23-MAN-1992

PRIOR APPLICATION NUMBER: US 07/35,064

FILING DATE: 10-UL-1991

RESISTRATION NUMBER: 35,030

REFERENCE/ORDIN NUMBER: 35,030

TELECOMMUNICATION NUMBER: 35,030

REFERENCE/ORDIN NUMBER: 35,030

TELECOMMUNICATION NUMBER: 35,030

REFERENCE/ORDIN NUMBER: 35,030

REFERENCE/ORDIN NUMBER: 35,030

REFERENCE/ORDIN NUMBER: 35,030

TELECOMMUNICATION NUMBER: 35,030

REFERENCE/ORDIN NUMBER: 35,030

REFERENCE/OR
```

ö

```
US-08-476-349A-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                             g
                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                     ;
0
                                                                                                                                     Gaps
                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                   Recombinant Antibodies for Human Therapy 114
                                                                                                           Length 123;
                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
                                                                                                                                     5,
                                                                                                         ore 46; DB 1;
ed. No. 3.9;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                          SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995
N: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      012712-161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VH5 clone 5-11
                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22313-140-
ZIP: 22313-140-
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NIMED FITTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
                                                                                                          Score
Pred.
                                                                                                                                                                                                                     RESULT 2
US-08-476-349A-82
; Sequence 82, Application US/08476349A
...+ont No. 5750105
                                                                   clone
                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                             Roland A.
                                                                                                                                                                                                                                                                               MATILL
Newman, Kull
Hanna, Nabil
Pecombi
                                                                                                          46.9%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                      SEE: BURNS, DOANE, 699 Prince St.
                                                                  VH5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 amino acids
amino acid
    relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not relevant
                                                                                                                                    Conservative
                                                                                                                                                                                       36
                                                                                                                                                             5 CGIDFIIFWIFW 16
                peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide
                                                                                                                                                                                                                                                                                                                                                           ADDRESS:
                                                                                                                                                                                     CGFSFTGFWISW
                                                 POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                      APPLICANT: Hanna, Na
APPLICANT: Raab, Ror
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                            Query Match
Best Local Similarity
                                        Monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monkey
                                                                                                                                                                                                                                                                 Patent No. 5750105
GENERAL INFORMATION:
APPLICANT: Newman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POSITION IN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 0 CLASSIFICATION:
TOPOLOGY: not
MOLECULE TYPE: |
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE
ADDRESSEE: F
                                        ORGANISM:
                                                                             US-08-478-039-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                      25
                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                      d
                                                                                                                                                             ò
```

```
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NATIONAL PROPERTY.
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US93-08528-76
; Sequence 76, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF;
; NUMBER OF SEQUENCES: 348
                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 298;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.25
                                 5
                                                                                                                                                                                                                                                                                                                                           300
    ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
Score 46; DB Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
14;
                                                                                                                                                                                                                                                                                                                                           Suite
                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45;
Pred. No.
                                                                                                                                                                                                                                                                     JA48

JEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Strate: D.C.
COUNTRY: USA
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Vacuerent APPLICATION DATA:

APPLICATION NUMBER: US/08/118,270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MURPHY=2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/118,270 FILING DATE: 09-SEP-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/943,236 FILING DATE: 10-SEP-1992
                                                                                                                                               RESULT 3
US-08-118-270-76
Sequence 76, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
 46.9%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 60.0%; 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 10-SEP-199
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 amino acids
                                  Conservative
                                                                  16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kevin
                                                                                                CGFSFTGFWISW 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Townsend, Kev REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
                                                                  CGIDFIIFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIDFIIFWIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
Query Match
Best Local Similarity
Matches 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE:
US-08-118-270-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 6
                                                                                                 25
                                                                  Ŋ
```

```
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                          Best
                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robert
No. 5977322el High Affinity Human Antibodies to
Tumor Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                   3: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Townsend and Crew LL lero Center, Eighth Floor
                                  Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                 MURPHY=2 PCT
                                                                                                                                                                                        APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45;
Pred. No.
                           419 Seventh Street, N.W., Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MBER: US 60/000,238
14-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-665-202-45
; Sequence 45, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
                AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.9%;
larity 60.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          James D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two Embarcadero
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide
                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15
                 BROWDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIDFIIFWIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Schier,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||::||:|
211 GIDWFLFWVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marks,
                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-73
TELEX: 248633
INFORMATION FOR SEQ
                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE:
                                                                                       20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYP
PCT-US93-08528-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                         COUNTRY:
                           STREET:
CITY: W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High Affinity Human Antibodies
                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                Length 125;
                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1:0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/665,202
                                                                                                                                                                                                                                                                                                                             4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l and Crew LLP
Eighth Floor
                                                                                                                                                                                                                                                                                               5;
                                                                 REGISTRATION NUMBER: 38,498
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                               Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JUN-1996
N: 424
               APPLICATION NUMBER: US 60/000,250 FILING DATE: 15-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NIME FITTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Townsend
Center, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No. 5977322el |
Tumor Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 46, Application US/08665202
Patent No. 5977322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (415) 576-0200
415) 576-0300
SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                           42.9%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  James D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Two Embarcadero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-08-665-202-45
                                                                                                                                                                                                                                                                                                                                                         6 GIDFIIFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 13-JUN-2
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Marks, JanaPPLICANT: Schier, Ratific OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                     26 GYDFTTYWIAW
                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks,
APPLICANT: Schier
                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94111-3834
                                                               Hunter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                 STRANDEDNESS TOPOLOGY: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: ('INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-665-202-46
                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
CITY: S
                                                                                                                                                                                                                                                                                               Query Match
```

linear

; 0

Wed

```
US-08-483-151-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
CITY: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME:
  GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                      ;
0
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                              Sequence 49, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies
TITLE OF INVENTION: Tumor Antigens
                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 125;
                                         Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Version #1.30
                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
16؛
                                          DB
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02307E-061410
                                          Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/65,202
FILING DATE: 13-JUN-1996
CLASSIFICATION A44
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 51, Application US/08665202
Patent No. 5977322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38,498
                                       42.9%;
ilarity 54.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.9%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acids
                                                                                                                                                                                                                                                                                                     141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16
peptide
                                                                                                                            36
                                                                                                 6 GIDFIIFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hunter, Tom
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                           San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIDFILFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | || :|| |
GYDFTTYWIAW
                                                                                                                   | || :|| GYDFTTYWIAW
                                                                                                                                                                                                                                                                                                                                           STREET: Two Embacity: San FrancisTATE: CaliforniCOUNTRY: USAZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                      Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
 TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
; MOLECULE TY;
US-08-665-202-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-08-665-202-51
                                                                                                                                                                                  US-08-665-202-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -08-665-202-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ဖ
                                                                                                                             26
                                           Query Match
                                                       Best_Local
Matches
                                                                                                                                                                        RESULT
                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
```

```
Gaps
                                  Ç
                               No. 5977322el High Affinity Human Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Seed, Brian
TITLE OF INVENTION: FUCOSYLTRANSFERASE GENES AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & pinh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                  Crew LLP
                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLI STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38,498
sr: 02307E-061410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42;
Pred. No.
                                                                                                                                                                                                                                                                 13-JUN-1996
13-JUN-1996
N: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
                                                                                                                                                                                                                                                                                                                                                                                                        IS-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCE ADDRESS:
1: Fish & Richardson P.C.
225 Franklin Street
                                                 Tumor Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 51
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.9%;
illarity 54.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 15-JUN-1995 ATTORNEY/AGENT INFORMATION:
  James D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acids
                  Robert
                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 13-JUN-19
CLASSIFICATION: 424
                                                                   141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIDFIIFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 GYDFTTYWIAW 36
APPLICANT: Marks, Ja
APPLICANT: Schier, R
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application Patent No. 5858752
GENERAL INFORMATION:
APPLICANT: Seed, Bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
`~~ 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE:
US-08-665-202-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS TOPOLOGY: 1
```

```
TITLE OF INVENTION: MOUSE NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardn STREET: 3000 K Street, N
                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 119 amino TYPE: amino acid
                                                                      Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RY: USA
20007-5109
                                                                                               COUNTRY: USA
ZIP: 20007-5109
                                                                                                                                                                                                                      FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE:
US-08-318-157B-2
                                                                                    D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-08-318-157B-12
                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
CITY: Wa
STATE: D
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STAPHYLOCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown.
                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                above locations
                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hans J.
Kathryn L.
CDR-GRAFTED TYPE III ANTI-CEA HUMANI:
                                                                                                                                                                                                                                                                                        Length 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 518
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
    PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ж
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at
                                                                                                                                                                                                                                                                                       ore 42; DB;
ed. No. 45;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ore 42; DB ed. No. 69; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid
                                                                                                            00786/278001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                       Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4069, Application US/09134001C Patent No. 6380370
                               US/08/483,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epidermidi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08318157B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
                                                                                                         REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                   5
                                                                                                35, 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of
            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,23
                                       07-JUN-1995
N: 530
                                                                                                                                                                                                                                                                                       42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.9%;
                                                                                                                                                                              ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identity
                                                                                                                                                                                                         342 amino acids
ino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::|||| | || RSNCGIGFKGFW 186
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                          SEQUENCE CHARACTERISTICS LENGTH: 342 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QANCGIDFILFW 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus
                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                             16
                                                                                                                                                                                                                                                                                                                                                                       31
                                                                                                                                                                                                                                                                                                                                             6 GIDFIIFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application Patent No. 5874540 GENERAL INFORMATION:
                                                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID
                                                                                                                                                                                                                                                                                                                                                                      GATEMVIWEEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HANSEN,
APPLICANT: ARMOUR,
TITLE OF INVENTION:
                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                     Similarity 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Lynn Dou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION:
US-09-134-001C-4069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: UNSURE
                                                                                                                                                                                                                      amino
                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                             -001C-4069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ
SEQ ID NO 4069
LENGTH: 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-318-157B-2
    SOFTWARE:
                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                            US-08-483-151-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175
                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                      Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-09-134-
                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Д
                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
Kathryn L.
CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
MOUSE MONOCLONAL ANTIBODIES
5 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                             #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
9
ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB
Pred. No. 21;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                         500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ., ve. 05/08/318,157B 05-0CT-1994 N: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 2000/-510.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CONTWARE: Patentin Release #1.0, Ve
MOUSE MONOCLONAL 58
                                                                         Suite
                                                                                                                                                                                                                                                             APPLICATION DATA:
APPLICATION NUMBER: US/08/318,157B
FILING DATE: 05-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/464
                                                                                                                                                                                                                                                                                                                                                                         28,665
:R: 18733/464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-U8-318-12/B-14
; Sequence 12, Application US/08318157B
; Patent No. 5874540
; GENERAL INFORMATION:
    APPLICANT: HANSEN, Hans J.
    APPLICANT: ARMOUR, Kathryn L.
    TITLE OF INVENTION: CDR-GRAFTED TYPE
    TITLE OF INVENTION: MOUSE MONOCLONAI
    NUMBER OF SEQUENCES: 58
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Foley & Lardner
    STREET: 3000 K Street, N.W., Suite
                                                                                                                                                                                                   IBM PC compatible YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
                                                      Lardner
set, N.W.
                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 42.9%; 6; Conservative
                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 ANCGIDFIIFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 AASGFDFTTYWMSW
```

ö

Gaps

```
-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-08-665-202-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                  -202-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ğ
                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                           Hans J.
Kathryn L.
CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
MOUSE MONOCLONAL ANTIBODIES
                                                                                                                                                                                 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 119;
                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,157B
FILING DATE: 05-OCT-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/464
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEFAX: (202)672-5399
TELEFAX: 904136
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                 ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                ore 41; DB ed. No. 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suite
                                                                                                                                                                                                                                                                                                     RESULT 13
US-08-318-157B-17
; Sequence 17, Application US/08318157B
; Patent No. 5874540
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; APPLICANT: ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED. TYP!
; TITLE OF INVENTION: MOUSE MONOCLONA!
                                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS: ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                            4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
TELECOMMUNICATION INFORMATION:
                                                      12:
                                                                                                                                                                               41.8%; 35.7%;
            (202)672-5300
(202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.8%; 35.7%;
                                     TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                   3 ANCGIDFIIFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 ANCGIDFIIFWIFW 16
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                    SSSGFDFTTYMMSW
                                                                                                                                      ; MOLECULE TYPE: protein US-08-318-157B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSSGFDFTTYWMSW
                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
5; Conserv
                                                                                                                                                                                           Local Similarity
hes 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
TOPOLOGY: LL.
                                                                                                          STRANDEDNESS
           TELEPHONE:
TELEFAX: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYP
US-08-318-1578-17
                                                                                                                          TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                               23
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Loc
Matches
                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ţ
                                                                                           High Affinity Human Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High Affinity Human Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                        L: Two Embarcadero Center, Eighth Floor
San Francisco
: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l and Crew LL
Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                13-JUN-1996
N: 424
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Townsend
Center, E
                                                                                         TITLE OF INVENTION: No. 5977322el TITLE OF INVENTION: Tumor Antigens NUMBER OF SEQUENCES: 141 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322e1
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
Sequence 48, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 50, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.8%; 54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESSEE: Townsend and TET: Two Embarcadero C: San Francisco
E: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 576-0 INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIDFILFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 GYDFSTYWIAW
                                                                        APPLICANT: Schier,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                          94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hunter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
S-08-665-202-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS
                                                                                                                                                        ADDRESSEE:
STREET: TW
CITY: San
STATE: Cal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
STREET: TW
CITY: San
STATE: Cal
```

us-09-854-133-587.rai

```
COMPUTER REALABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: INB PC Compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 13-UN-1995
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UN-1995
APPLICATION NUMBER: US 60/000
FILING DATE: 15-UN-1995
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UN-1995
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-UN-1995
APPLICATION NUMBER: US 60/000,250
FILING DATE: US 60/000
FILING DATE: US
```

```
5.1.6
Compugen Ltd.
 version
- 2003
GenCore
(c) 1993
        Copyright
```

model using sw search, protein OM protein

Seconds Search time 5.38053 Solithout alignments) 346.196 Million cell •• 2003, 15:06:38 σ July Run on:

updates/sec

US-09-854-133-587 98 score: Perfect Title:

FQANCGIDFILFWIFW Sequence:

Gapext BLOSUM62 Gapop 10.0 table: Scoring

5

0

445758 segs, 116419773 residues Searched:

445758 parameters hits satisfying chosen of Total number

length: 0 length: 2000000000 sed DB DB Minimum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

icted by chance to have a sof the result being printed, score distribution. predicted by score of the the total reater than or equal to the derived by analysis of the greater Š Pred. N score g and is

SUMMARIES

Result		% Query				
-	Score	Match	Length	DB	ΠD	Description
	98	00.	16	σ	US-09-854-133-587	Sequence 587, App
		00	16	σ	US-10-144-649A-587	587,
_		00	16	10	US-09-738-973-587	Ψ
		00	97	σ	-58	586,
		00	97	თ	9A-58	586,
		•	97	10	US-09-738-973-586	w
_		00	114	σ	74	74
<u>~</u>		•	64	10	18	e 1
_	46	46.9	123	10	US-09-850-165-90	Sequence 90, Appl
_		•	323	σ	US-10-266-643-4	4
		•	323	10	0 US-09-816-087-4	() 4
~		•	343	თ	US-10-176-079-2	Sequence 2, Appli
ω.		•	343	σ	US-10-176-079-9	σ
		•	343	σ	US-09-929-752-2	2
ın		•	343	σ	US-09-929-752-9	Sequence 9, Appli
'n		•	343	σ	US-10-225-567A-482	48
_		•	343	σ	US-10-184-426-2	7
_		•	343	6	US-10-184-426-9	9
_		•	343	10	US-09-985-694A-2	٥

Sequence 9, Appli Sequence 973, App Sequence 11503, A Sequence 1138, App Sequence 1138, App Sequence 132, Appli Sequence 1073, Ap Sequence 1073, Appli Sequence 1073, Appli Sequence 17, Appli Sequence 17, Appli Sequence 5746, Appli Sequence 5146, Appli Sequence 51, Appli Sequence 610, Appli Sequence 881, Appli Sequence 100, Appli Sequence 9, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli
10 US-09-985-694A-9 9 US-09-925-299-973 10 US-09-925-299-973 10 US-09-815-242-11503 9 US-09-815-242-11388 10 US-09-815-242-11388 10 US-09-815-242-11388 10 US-09-784-077-2 10 US-09-784-077-2 10 US-09-789-561-132 10 US-09-789-561-132 10 US-09-729-094-4 9 US-10-091-504-17 10 US-09-253-794-17 9 US-09-253-794-17 9 US-09-253-794-17 10 US-09-253-794-10 10 US-09-253-794-9 10 US-09-253-794-9 10 US-09-253-794-10 10 US-09-253-794-11 10 US-09-253-794-11 10 US-09-253-794-11
33 33 33 33 33 33 33 33 33 33 33 33 33
444444444444444444444 ?%%%%%%%%%%%%%%%%
4 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

```
RESULT 1
US-09-854-133-587

; Sequence 587, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Henderson, Darin R.
; APPLICANT: Benson, Darin R.
; APPLICANT: Benson, Darin R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER;
; TITLE OF INVENTION UMBER: US/09/854,133
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOOTHWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 98; DB 9; Pred. No. 1.5e-08; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    th 100.08; Similarity 100.08; 16; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FQANCGIDFIIFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-854-133-587
                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 587
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
```

RESULT 2
US-10-144-649A-587
; Sequence 587, Application US/10144649A
; Publication No. US20030118599A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Algate, Paul A.
; APPLICANT: McNeill, Patricia D. FOANCGIDFILFWIFW 16 ΩQ

ö

Gaps

ö

```
; ORGANISM: HOMO US-10-144-649A-586
                                                                                                                                                                                                                                                                                                                               US-10-144-649A-586
                                                                               SEQ ID NO 586
LENGTH: 97
                                                                                                                                                                          Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35
                                                                                                               PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT
APPLICANT
APPLICANT
APPLICANT
APPLICANT
APPLICANT
APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Matc|
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT
                                                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qγ
                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Indirias, Carol Yoseph
APPLICANT: Benson, Darin R.
APPLICANT: Elliot, Mark
APPLICANT: Mannion, Jane
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
                    CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 16;
                                                                                                                                                                                                       Length 16;
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG FILE REFERENCE: 210121.475C11
CURRENT APPLICATION NUMBER: US/10/144,649A
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 749
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 16
                                                                                                                                                                                         DB 9; Le
1.5e-08;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 98; DB 10;
Pred. No. 1.5e-08;
Mismatches 0;
                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 210121.475C9
CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                     Score 98;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                          US/09738973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09854133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-854-133-586
; Sequence 586, Application US/0985413
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AN.
; TITLE OF INVENTION: THE THERAPY AN.
                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ø
                                                                                                                                                                                                     100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                Reed, Steven G.
Henderson, Robert P
Lodes, Michael J.
Fling, Steven P.
Mohamath, Raodoh
Algate, Paul A.
Secrist, Heather
Indirias, Carol Yos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                   1 FQANCGIDFILFWIFW
                                                                                                                                                                                                                                                                                 1 FOANCGIDFILFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOANCGIDFIIFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOANCGIDFILFWIFW
                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-09-738-973-587
; Sequence 587, Application US
; Patent No. US20020110563A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                        ; ORGANISM: Homo sapiens US-10-144-649A-587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens -09-738-973-587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
16; Conserv
                                                                                                                                                                                                                   Best Local Similarity
Matches 16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Fa
SEQ ID NO 587
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₩
                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 586, Application US/10144649A
Publication No. US20030118599A1
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Algate, Paul A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.475C11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mannion, Jane
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C9
CURRENT APPLICATION NUMBER: US/09/738,973
                                                                                                                                                                                                  Length 97;
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.8e-08;
                                                                                                                                                                                                 Score 98; DB 9;
Pred. No. 7.8e-08
Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ο</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/144,649A
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 749
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-738-973-586

; Sequence 586, Application US/09738973

; Patent No. US20020110563A1

; GENERAL INFORMATION:

; APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yoseph
                                                                                                                                                                                                 th 100.0%; Similarity 100.0%; 116; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reed, Steven G.
Henderson, Robert A.
Lodes, Michael J.
Fling, Steven P.
Mohamath, Raodoh
Algate, Paul A.
Secrist, Heather
Indirias, Carol Yoseg
Benson, Darin R.
Elliot, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
100.0%;
                                                                                                                                                                                                                                                                       1.6
                                                                                                                                                                                                                                                                                        35 FQANCGIDFILEWIEW 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16
                                                                                                                                                                                                                                                                       1 FQANCGIDFIIFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FOANCGIDFIIFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FQANCGIDFILFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-854-133-586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Similarity
16; Conser
```

```
ö
                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LUNG CANCE
                                                                                                                                            Length 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Fan, Liqun
APPLICANT: Algate, Paul A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUN
FILE REFERENCE: 210121.475C11
CURRENT APPLICATION NUMBER: US/10/144,649A
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 749
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                            Score 98; DB 10;
Pred. No. 7.8e-08;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 98; DB 9;
Pred. No. 9e-08;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1842, Application US/09925300

Sequence 1842, Application US/09925300

Batent No. US20020151681A1

GENERAL INFORMATION:

APPLICANT: Craig Rosen,

APPLICANT: Steve Ruben

TITLE OF INVENTION: Nucleic Acids, Proteins and
FILE REFERENCE: PA101

CURRENT APPLICATION NUMBER: US/09/925,300

CURRENT FILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1842

LENGTH: 64
          NUMBER OF SEQ ID NOS: 587
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 586
LENGTH: 97
                                                                                                                                                                                                                                                                                                          Sequence 742, Application US/10144649A Sequence 742, Application US/10144649A Publication No. US20030118599A1 GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                              ;
0
2000-12-14
                                                                                                                                             100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67
                                                                                                                                                                                                                 1 FQANCGIDFILFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FOANCGIDFIIFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 FQANCGIDFILFWIFW
                                                                                                                                                                                                                                FOANCGIDFILFWIFW
                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-10-144-649A-742
                                                                                               ; ORGANISM: Homo sapiens US-09-738-973-586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 16; Conservation
                                                                                                                                                               Similarity
CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: HOMO US-09-925-300-1842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-925-300-1842
                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : PRT
                                                                                                                                                                                                                                                 35
                                                                                                                                                 Query Match
                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best
                                                                                                                                                                                                                                                                                                RESULT
US-10-1
                                                                                                                                                                Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ω
                                                                                                                                                                                                                Qγ
                                                                                                                                                                                                                                                 g
```

```
ö
                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10266643

Publication No. US20030059891A1

GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui

TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

FILE REFERENCE: CL000749-CON

CURRENT APPLICATION NUMBER: US/10/266,643

CURRENT FILING DATE: 2002-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: monkey clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 123;
 Length 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                    Indels
                                                                                                                                                                                                                                 GENERAL INFORMAN, ROLAND A.

APPLICANT: HANNA, NABIL
APPLICANT: HANNA, NABIL
APPLICANT: RAAB, RONALD W.
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THE
FILE REFERENCE: 037003-0280614
CURRENT APPLICATION NUMBER: US/09/850,165
CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: 09/082,472
PRIOR FILING DATE: 1998-05-21
PRIOR FILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: 08/476,237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5,
                                     ..
H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.9%; Score 46; DB larity 58.3%; Pred. No. 7.3; Conservative 0; Mismatches
Score 46; DB Pred. No. 4; S; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1992-07-10
PRIOR APPLICATION NUMBER: 07/856,281
PRIOR FILING DATE: 1992-03-23
PRIOR APPLICATION NUMBER: 07/735,064
PRIOR FILING DATE: 1991-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TUMBER: 07/912,292
1992-07-10
TUMBER: 07/856,281
                                                                                                                                                                                               90, Application US/09850165
0. US20020150580A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
 46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-266-643-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 CGIDFIIFWIFW 16
                 Similarity 50.06; Conservative
                                                                      QANCGIDFIIFW 13
                                                                                           ::|||:||: |:
ESNCGLDFVSFF 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGFSFTGFWISW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 7; Conser
                                                                                                                                                                                                 Sequence 90, Applica
Patent No. US2002015
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 4
                                                                                                                                                              RESULT 9
US-09-850-165-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q ID NO 90
LENGTH: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-266-643-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
                                                                                                           29
                                                                         7
   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE
                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                         QΥ
                                                                                                            g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>;</u>
                                                                                                                                                                                                                                         HUMAN GPCR
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                      Sequence 4, Application US/09816087

Sequence 4, Application US/09816087

GENERAL INFORMATION:

APPLICANT: WEI, Ming-Hui

TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING;

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

FILE REFERENCE: CL000749-CIP

CURRENT APPLICATION NUMBER: US/09/816,087

CURRENT FILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                        NG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 323;
    Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 343;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10176079

Sequence 2, Application US/10176079

Publication No. US20020192760A1

GENERAL INFORMATION:

APPLICANT: Li et al.

TITLE OF INVENTION: G-Protein Coupled Receptor

FILE REFERENCE: PF145P1D1C1

CURRENT APPLICATION NUMBER: US/10/176,079

CURRENT FILING DATE: 2002-06-21

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 1995-06-05

PRIOR FILING DATE: 1994-11-18

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                              10;
    DB 9;
25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 1
Pred. No. 25;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45; DB 9
Pred. No. 27;
3; Mismatches
                      ed. No. 25;
Mismatches
    Score 45;
Pred. No. 2
                                3
                                                                                                                                                                                                                                                                                                                                                                                                                                                       3
                                                                                                                                                                                                                                                                                                                                                                                                                          45.9%;
illarity 60.0%;
Conservative
Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.9%;
llarity 60.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Rattus norvegicus US-09-816-087-4
                                                                          |||::||:|
244 GIDWFLFWVF 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265
                                                            15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 GIDFIIFWIF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
                                                           GIDFILFWIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||: :||:|
GIDWFLFWVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 GIDFIIFWIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIDWFLFWVF
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: human
US-10-176-079-2
                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 4
LENGTH: 323
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFIWALL SEQ ID NO 2
                                                                                                                                             US-09-816-087-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-176-079-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -079-9
                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-10-176-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hinuma, Shuji
Fujii, Ryo
Kawamata, Yuji
NVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
PRODUCTION AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                            Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/929,752
FILING DATE: 14-Aug-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/555,905
                                           APPLICANT: Li et al.

TITLE OF INVENTION: G-Protein Coupled Receptor
FILE REFERENCE: PF145P1D1C1

CURRENT APPLICATION NUMBER: US/10/176,079

CURRENT FILING DATE: 2002-06-21

PRIOR APPLICATION NUMBER: 09/562,909

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 1995-06-05

PRIOR FILING DATE: 1995-06-05

PRIOR FILING DATE: 1994-11-18

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 28-DLC
APPLICATION NUMBER: JP 7-UC
FILING DATE: 20-JAN-1995
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
FILING DATE: 16-MAR-1995
FILING DATE: 10-AUG-1995
TAMES: 10-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                              27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: <Unknown>
APPLICATION NUMBER: JP 7-215798
FILING DATE: 24-AUG-1995
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                           Score 45;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-09-929-752-2
; Sequence 2, Application US/09929752
; Publication No. US20030113909A1
; GENERAL INFORMATION:
. APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
Sequence 9, Application US/10176079 Publication No. US20020192760A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                              ä;
                                                                                                                                                                                                                                                                                                                                                                                           45.9%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 GIDFILFWIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||: :||:|
256 GIDWFLFWVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                      ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF
                                                                                                                                                                                                                                                                                                      343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER
                                                                                                                                                                                                                                                                                                                                                        US-10-176-079-9
                                                                                                                                                                                                                                                                                                                       PRT
                                                                                                                                                                                                                                                                                    SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                       TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \overline{\mathbf{p}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δy
```

27,026

```
;
0
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                           Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             & CUSHMAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL INFORMAT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
Fujii, Ryo
Kawamata, Yuji
TITLE OF INVENTION: G PRODUCTION AND USE THEREOF
                                                                                                                                                                                                                                                                            σì
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 1550/45836
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROBERTS
   1550/45836
                                                                                                                                                                                                                                                                          DB
27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION DATA:
APPLICATION NUMBER: US/09/929,752
FILING DATE: 14-Aug-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/55,905
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 7-215798
FILING DATE: 24-Aug-1995
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
APPLICATION NUMBER: JP 7-224544
FILING DATE: 10-Aug-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER: US/09/929,752
14-Aug-2001
                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                          Score 45;
Pred. No.
                                                                                                                                                                                                                       \alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN,
STREET: 130 Water Street
                                                                                                                                                                                                                        SEQ ID NO:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-09-929-752-9
; Sequence 9, Application US/09929752
; Publication No. US20030113909A1
; GENERAL INFORMATION:
                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Conlin, David G. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                            45.9%;
60.0%;
                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: S

US-09-929-752-2
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                  15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 130 W
CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                   GIDFIIFWIF
                                                                                                                                                                                                                                                                                                                                                                      256 GIDWFLFWVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02109
                                                                                                                                                                                                                                                                                            Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                             Best_Local
Matches
                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                   õ
```

```
ö
                                                                                      Gaps
                                                                                     ö
                                                                 Length 343;
                                                                                      Indels
                                                                  9;
                                                         DB . 27.
                                                                                     Mismatches
                                                                  Score 45;
Pred. No.
                                       Φ
                                       SON.
                                                                                                                                                        9, 2003, 15:10:29
;
STRANDEDNESS: <Unknown>
;
TOPOLOGY: linear
;
MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID
US-09-929-752-9
                                                                                     3;
                                                                 45.9%;
illarity 60.0%;
Conservative
                                                                                                          6 GIDFIIFWIF 15
                                                                                                                    |||: :||:|
GIDWFLFWVF
                                                                                                                                                      completed: July ne : 6.38053 secs
                                                                            Best_Local Similarity
Matches 6; Conser
                                                                                                                           256
                                                                   Query Match
                                                                                                                                                         Search co
                                                                                                          δy
                                                                                                                            qq
```

			•	•	
					§ -
				•	
		•			
				•	
•		49			
	•				
			e de		
					š ,
					i

```
5.1.6
Compugen Ltd
GenCore version
Copyright (c) 1993 - 2003
```

using sw model OM protein - protein search, 9, 2003, 15:05:28 ; Search time 7.22124 Seconds (without alignments) 213.004 Million cell updates/sec July Run on:

1 FOANCGIDFIIFWIFW 16 US-09-854-133-587 98 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

,	ript	ALG6 protein - year	membrane glyco	DH2 dehydrogen	otein-coupled		reducta	s a	NADH2 dehydrogenas	permea	amino acid permeas	l prot	+ 1200		- שנופ	וויק [מני	יה ליר	ל מיל המיל	Forhrome.c	heavy chain V	heavy chain V	heavy chain	chain V	Pase subunit 6	oothetical pro	lic acid transp	onthetical pr	pocificat process	i prot	1 prot
SUMMARIES	ID	1 00	C	D95366	α	$\boldsymbol{\sigma}$	$\boldsymbol{\sigma}$	_	10	\sim	-	\sim		1O	10	\sim	10		S41689	\sim	$\overline{}$	81	142	1107	542	6439	2558	2594		7116
	\Box	7	г ,	7	N	Н	7	7	7	7	П	7	Н	7	~	7	7	-	~	7	7	7	7	7	7	7	7	Н	7	7
	4	544	Ψ	O	4	~	σ	æ	(L)	-	-	4	0	$^{\circ}$	7	σ	ഹ	\sim	483	\sim	$^{\circ}$	\sim	3	O)	ᇜ	₹*	₹*	ത	CO)	\sim
di	Query Match	51.0	φ.	٠	Ŋ.	4.	•	س	ب	<u>ښ</u>	ж	щ	ω,	ď	ά.	2	ζ.	2	42.9	1.	1.	H.	-	급.	1.	┧.	Ξ.	H	₽.	-
	a) i	50	48	47	45	44	44	43	43	43	43	43	43	42	42	42	42	42	42	41	41	41	41	41	41	41	41	41	41	40.5
	Result No.	Н	7	m	4	വ	9	7	&	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

al prot	het ic	hetical pro	tical pro	pothetical pro	eavy chain V	hetical prot	sugar tr	ble membrane	hetical 37.	thetical prot	thetical prot	bable membrane	thetical prot	othetical pro
AD2556 859109	4782	8472		381	625	87	9698	048	4774	117	602	960	421	8622
0.0	1 (1	7	7	7	Ň	7	7	7	~	~	7	7	~	7
318	אל		70	46	1.19	221	289	309	337	m	337	342	375	378
41.3			•	•	•	•								
40.5	0	0	. 40	40	40	40	40	40	40	40	40	40	40	40
	2								_					

ALIGNMENTS

4 NCGIDFIIFWIFW 16 ||:||:||| 514 NCAVGFICFSIFW 526

ōy

qq

N; Alternate

ö

Gaps

; 0

and tis

sequencing,

D.R.; LY

GB: M3209

ô

Gaps

ô

```
Conserved hypothetical protein yndM - Bacillus subtilis
C)Species: Bacillus
C)Species: C)Species: Bacillus
C)Species: C)Species: Bacillus
C)Species: C)Species: Bacillus
C)Species: C)Sp
                                                                                                                                                                                                                                                                                                             G protein-coupled receptor RTA - rat
C; Species: Rattus norvegicus (Norway rat)
C; Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Jul-1999
C; Accession: A35639
R; Ross, P.C.; Figler, R.A.; Corjay, M.H.; Barber, C.M.; Adam, N.; Harcus, D.R.
Rross, P.C.; Figler, R.A.; Corjay, M.H.; Barber, C.M.; Adam, N.; Harcus, D.R.
Proc. Natl. Acad. Sci. U.S.A. 87, 3052-3056, 1990
A; Title: RTA, a candidate G protein-coupled receptor: cloning, sequencing, and
A; Reference number: A35639; MUID:90222168; PMID:2109324
A; Reference number: A35639
A; Molecule type: mRNA
A; Residues: 1-343 <ROS>
A; Cross-references: GB:M35297; NID:g206809; PIDN:AAA42087.1; PID:g206810; GB:M
C; Superfamily: mas transforming protein
C; Superfamily: mas transforming protein
C; Keywords: G protein-coupled receptor; glycoprotein; membrane protein
F; 4/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                     #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ed. No. 15;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.9%; Score 44; DB 46.2%; Pred. No. 12; Live 4; Mismatches
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.9%;
ilarity 60.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |: |: |: |:|
94 ADFGLSFVILWVF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 ANCGIDFILFWIF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
      Conservative
                                                                                                                                             CALDLFLFYVFW 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265
                                                                      5 CGIDFIIFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 GIDWFLFWVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conser
5
                                                                                                                                             127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
Matches
      Matches
                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Noblections (ubiquinone) (EC 1.6.5.3) NuoM2 [imported] - Sinorhizobium meliloti (Species: Sinorhizobium meliloti (C) Species: Spe
                                                                                                                                                                                                                                                                                                                                                                                                             genomic RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                 coronavirus
                                                                                                                                                                                                                                                               16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PID:9406200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           te (Asn) (covalent) #status predicted
te (Ser) (covalent) #status predicted
(Thr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                 canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Molecule type: genomic RNA
A; Residues: 1-262 <HOR>
A; Residues: 1-262 <HOR>
A; Cross-references: DDBJ:D13096; NID:g406193; PIDN:BAA02413.1; P
C; Genetics:
A; Gene: M
C; Superfamily: coronavirus E1 membrane glycoprotein
C; Superfamily: signal sequence #status predicted <SIG>
F; 1-17/Domain: signal sequence #status predicted <ANA
F; 18-262/Product: E1 membrane glycoprotein #status predicted <AMA
F; 56-72/Domain: transmembrane #status predicted <TM1>
F; 85-101/Domain: transmembrane #status predicted <TM2>
F; 115-134/Domain: transmembrane #status predicted <TM3>
F; 32,55/Binding site: carbohydrate (Ser) (covalent) #status predict
F; 44/Binding site: carbohydrate (Thr) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 491;
                                                                                                                                                       (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 262;
                                                                                                                                                                                                                                                               #text_chang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN:BAA02413.1
                                                                                                                                                                                                                                                                                                                                                                                                           οĘ
                                                                                                                                                                                                                                                                                      C; Accession: JQ1724
R; Horsburgh, B.C.; Brierley, I.; Brown, T.D.K.
J. Gen. Virol. 73, 2849-2862, 1992
A; Title: Analysis of a 9.6 kb sequence from the 3' end characterence number: PQ0481; MUID:93057357; PMID:1431811
A; Accession: JQ1724
                                                                                                                                                       coronavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chain
                                                                                                                                                                                                                                                               17-Feb-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (upidniuone)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; Pred. No.
                                                                                                                                                     canine
                                                                                                                                                 l membrane glycoprotein precursor - ca
Alternate names: matrix glycoprotein
Species: canine coronavirus
Date: 17-Feb-1994 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Superfamily: NADH dehydrogenase;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGIDFILFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Contents: annotation C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid
```

Ŋ

ö

Query Match

Matches

81

qq

RESULT

ö

Gaps

.; 0

Query Match Best Local

ene: nuoM2

Genome:

```
A; Residues: 1-332 <PAR>
A; Residues: 1-332 <PAR>
A; Cross-references: GB:AL139079; GB:AL111168; NID:g6968971; PIDN:CAB73560.1; PID:g6
A; Experimental source: serotype O2, strain NCTC 11168
C; Genetics:
A; Genetics:
A; Genetics:
C; Guperfamily: NADH dehydrogenase (ubiquinone) chain 1
C; Superfamily: NADH dehydrogenase (ubiquinone) chain 1
C; Keywords: membrane-associated complex; NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB:AE001439; NID:g4154929; PIDN:AAD05979.1; PID:g4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid permease (rocE) - Helicobacter pylori (strain 26695)
C; Species: Helicobacter pylori
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: A64647
C; Accession: A64647
C; Accession: A64647
C; Accession: A64520; MUID: 97394467; PMID: 9252185
A; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Frase A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A; Reference number: A64520; MUID: 97394467; PMID: 9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB:AE000511; NID:g2314160; PIDN:AAD08062.1; PID:g2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Helicobacter pylori
A; Variety: strain J99
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Aug-1999
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Aug-1999
C; Accession: A71937
R; Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; S; Alm, R.A.; Ling, L.S.L.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vature 397, 176-180, 1999
A; Title: Genomic sequence comparison of two unrelated isolates of the human A; Reference number: A71800; MUID: 99120557; PMID: 9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                ó.
                                                                                                                                                                                                   332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glycoprotein; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     399)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; nucleic acid sequence not A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ore 43; DB ] ed. No. 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB Pred. No. 40; 5; Mismatches
                                                                                                                                                                                                 Score 43; DB Pred. No. 30; 0; Mismatches
                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                    permease - Helicobacter pylori
Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB:AE001474; (A; Experimental source: strain J99 C; Genetics: A; Gene: jhp0406 C; Superfamily: arginine permease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-519 <TOM>
A; Cross-references: GB:AE000610; (C; Superfamily: arginine permease C; Keywords: amino acid transport;
                                                                                                                                                                                                43.9%;
ilarity 75.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.9%;
llarity 36.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 43.9%;
Local Similarity 36.4%;
nes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGYMVFWMYW 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                                                                                                     287 FIFFWYFW 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIDFILFWIFW
                                                                                                                                                                                                                                                                                           16
                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
Les 4; Conser
                                                                                                                                                                                                                                                                                           FILFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
  DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type: D: 1-475
type: D: 1-332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                          Qγ
                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QΣ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bacter jejuni reveals hyp
                                                                                                                                                                                                                                                t-Producing Bacterium Cld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AH0415
C;Accession: AH0415
B;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AH0415
A;Accession: Lype: DNA
A;Residues: 1-284 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Campylobact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chillir
Chillir
                                                                                                                                                                               R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D.; C
                                                                                                                                                                              Zeng, Q.; Gibson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                 GSPDB:GN00168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSPDB:GN00175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.; Basham, 1
A.; Whitehead,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-Jun-2002
                                                                                                                                   14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                       icum
                                                                         Fe-S oxidoreductase CAC0765 [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-C; Accession: B96994
R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, J. Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Pr A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Accession: B96994
A; References preliminary
A; Molecule type: DNA
A; Residues: 1-391 <KUR>
A; Residues: 1-391 <KUR>
Cross-references: GB: AE001437; PIDN: AAK78741.1; PID:915023650; GS
A; Experimental source: Clostridium acetobutylicum ATCC824
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 Cj1572c [sC; Species: Campylobacter jejuni
C; Species: Campylobacter jejuni
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change
C; Accession: B81252
R; Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; Vanvliet, Rature 403, 665-668, 2000
A; Title: The genome sequence of the food-borne pathogen Campylok
A; Reference number: A81250; MUID:20150912; PMID:10588204
A; Accession: B81252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AL590842; PIDN:CAC92652.1; PID:g15981349
C;Genetics:
A;Gene: ampE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB Pred. No. 24; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.9%;
illarity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :| ||| |: |: |
184 RAQTGIDGILHWLDW 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 QANCGIDFIIFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :||:|| |::
101 SNCGVDFFDFYL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 ANCGIDFIIFWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              CAC0765
                                        ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 α
                                        RESULT
B96994
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
```

gastric

ö

ö

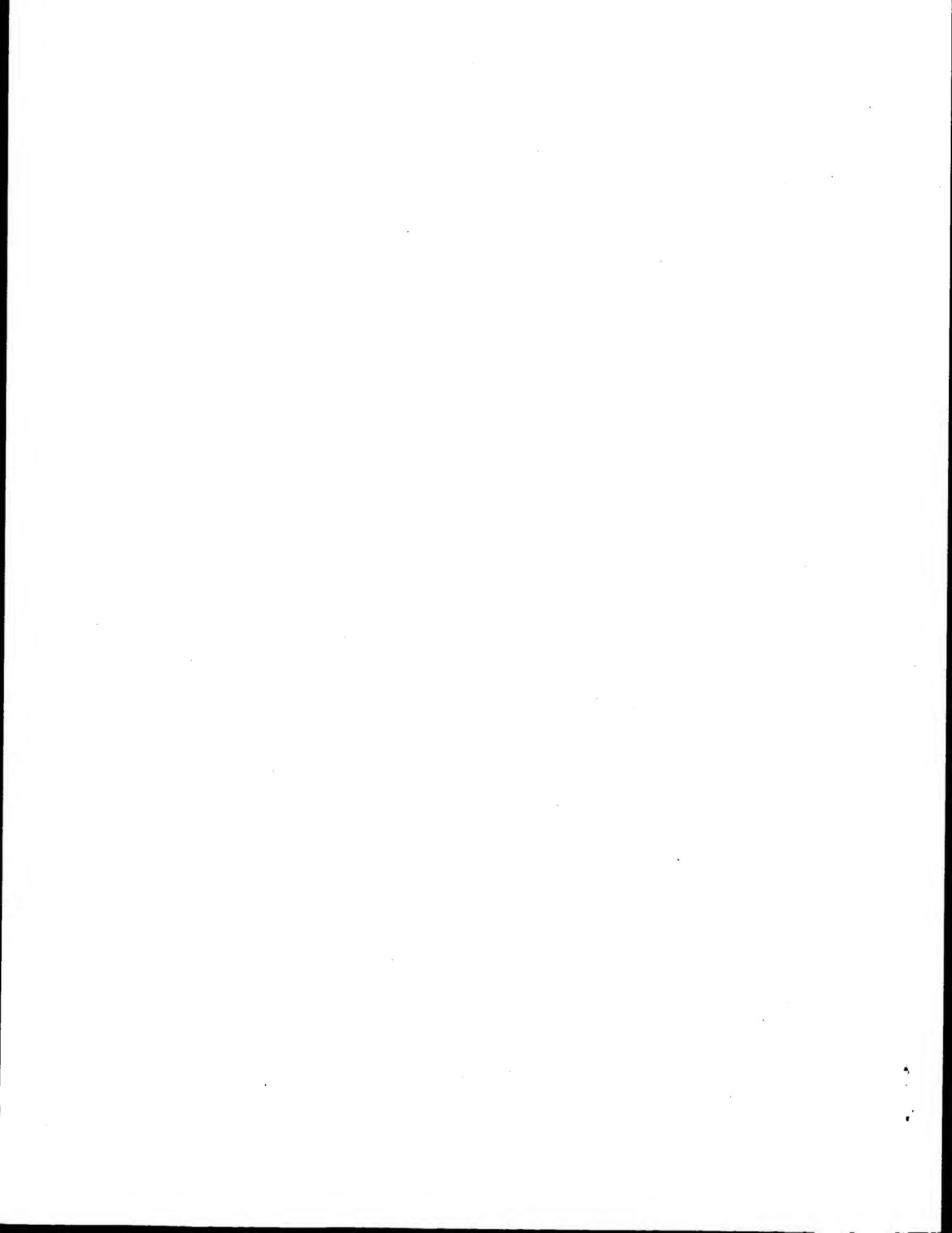
Smith, Vovis,

MO

ö

```
hypothetical protein all4113 [imported] - Nostoc sp. (strain PCC 7120)
C; Species: Nostoc sp.
A; Note: Nostoc sp.
A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C; Accession: AB2320
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irir
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabar
DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Reference number: AB2320
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-194 <KUR>
A; Residues: 1-194 <KUR>
A; Cross-references: GB:BA000019; PIDN:BAB75812.1; PID:g17133248; GSPDB:GN00179
A; Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSPDB:GN00007; MIPS:YGI
                                                     sequences and antigen binding specificity of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
S64252
probable membrane protein YGL230c - yeast (Saccharomyces cerevisiae)
N; Alternate names: hypothetical protein 60946
C; Species: Saccharomyces cerevisiae
C; Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
C; Accession: S64252
R; Fartmann, B:, Kramer, W.
Submitted to the Protein Sequence Database, May 1996
A; Reference number: S64248
A; Reference number: S64248
A; Molecule type: DNA
A; Residues: 1-147 < FAR>
A; Cross-references: EMBL:Z72752; NID:q1322886; PID:q1322887; GSPDB:GN00007; M1
A; Experimental source: strain S288C
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Cross-references: SGD:S0003199
A; Map position: 7L
C; Superfamily: Saccharomyces cerevisiae probable membrane protein YGL230c
C; Keywords: transmembrane protein
F; 89-105/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                               A; Reference number: A30560; MUID:89110062; PMID:2464028
A; Accession: A30560
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-121 <MAT>
A; Residues: 1-121 <MAT>
A; Cross-references: GB:M22955; NID:9195610; PIDN:AAA38368.1; PID:9195611
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                         Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 147
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4,
                                                                                                                                                                                                                                                                                                                                                                                                                             5,
                                                                                                                                                                                                                                                                                                                                                                       .;
?
                                                                                                                                                                                                                                                                                                                                                                       Score 42; DB;
Pred. No. 18;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB Pred. No. 21; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
21;
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 50.0%; 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | |||| :|: |
23 AASGIDFSRYWMSW 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 ANCGIDEILEWIEW 16
R;Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
A;Title: Variable region cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 CAIQFLFFIIYW 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGIDFILFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                       Ogud
K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
                                                                                                                                                                                               hypothetical protein araB [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: B89823
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
C; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Recession: B89823
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-545 <KUR>
A;Residues: 1-545 <KUR>
A;Residues: 1-545 <KUR>
A;Cross-references: GB:BA000018; PID:g13700443; PIDN:BAB41741.1; GSPDB:GN00149
A;Gene: araB
C;Superfamily: ribulokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  559/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Introns: 31/2; 72/3; 123/2; 187/3; 227/2; 299/3; 331/3; 389/3; 428/3; 484/; Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology; Keywords: glycosyltransferase; hexosyltransferase; keywords: glycosyltransferase; hexosyltransferase; 276-750/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D:916526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sedneuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sucrose synthase (EC 2.4.1.13) - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 11-.
C; Accession: S19125
R; Chopra, S.; Del-favero, J.; Dolferus, R.; Jacobs, M.
Plant Mol. Biol. 18, 131-134, 1992
A; Title: Sucrose synthase of Arabidopsis: genomic cloning and sequent A; Reference number: S19125; MUID: 92119221; PMID:1531031
A; Accession: S19125
A; Status: nucleic acid sequence not shown
A; Status: nucleic acid sequence not shown
A; Residues: 1-804 <CHO>
A; Cross-references: EMBL:X60987; NID:q16525; PIDN:CAA43303.1; PID:q1
C; Genetics:
A; Introns: 31/2; 72/3; 123/2; 187/3; 227/2; 299/3; 331/3; 389/3; 428
C; Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase
C; Keywords: glycosyltransferase; hexosyltransferase
C; Keywords: glycosyltransferase; hexosyltransferase
E; 276-750/Domain: sucrose/sucrose-phosphate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V region (16.4.12E) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change
C;Accession: A30560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ore 43; DB 1;
ed. No. 63;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB;
Pred. No. 45;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.9%;
llarity 62.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.9%;
larity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 RSNCGLGFKAFW 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 QANCGIDFIIFW 13
                                                                          GTGYMVFWMYW 147
                       GIDFILFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |: ||:||
19 FLSFWVFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 FIIFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 6
                       ဖ
                                                                         137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                         RESULT
B89823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A30560
                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
```

```
C;Genetics:
A;Gene: all4113
C;Superfamily: Synechocystis hypothetical protein sll1656
C;Superfamily: Synechocystis hypothetical protein sll1656
Query Match
Best Local Similarity 37.5%; Pred. No. 27;
Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
Qy 1 FQANCGIDFIIFWIFW 16
| | | | | ::| ::|
Db 70 FWAVCGVIALLFSVYW 85
Search completed: July 9, 2003, 15:09:49
Job time: 12.2212 secs
```



```
5.1.6
Compugen
 version
- 2003
GenCore
(c) 1993
       Copyright
```

model ΝS using search, protein protein Θ

Search time 1.9823 Seconds (without alignments) 334.773 Million cell upday 15:05:28 2003, 9 July ou: Run

updates/sec

16 FQANCGIDFIIFWIFW US-09-854-133-587 98 1 FQANCGIDFIIFWIF score: Sequence: Title: Perfect

Gapext BLOSUM62 Gapop 10.0 Ü table Scoring

0.5

residues 41476328 112892 segs, Searched:

112892 chosen parameters satisfying hits of number Total

length: 0 length: 2000000000 sed DB DB Minimum Maximum

Minimum Match 0% Maximum Match 10 Listing first 45 Post-processing:

100% 45 summaries

SwissProt_40:

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal terine score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

rattus norv drosophila staphylococ arabidopsis saccharomyc archaeoglob mus musculu methanococc marchantia chondrus cr escherichia mycoplasma rattus norv felis silve homo sapien sus scrofa escherichia porcine res porcine tra saccharomyc canine ente rattus norv mycoplasma treponema p mus musculu porcine res feline infe chloroflexu musculu musculu musculu lactococcus Description mns mus mus mus P36299 P23749 P83294 P83294 P83294 P0000917 P0000917 P26848 P47393 P18088 P18088 P18088 P18088 P18088 P18088 P18088 P1695 P01175 P01175 P01175 P01175 P01175 P011809 P011815 P011815 P011815 VME1_CVPPU VME1_CVPPU VME1_FIPV RCEL_CHLAU MRAY_LACLA YA85_MYCPN NADE_TREPA HV36_MOUSE HV36_MOUSE HV39_MOUSE HV37_MOUSE ALG6_YEAST
VME1_CVCAI
RTA_RAT
G64B_DROME
ARAB_STAAM
SUS2_ARATH
YGY0_YEAST
YL31_ARCFU
FUT7_MOUSE
Y762_METJA
NU4M_MARPO
NU5M_CHOCR
YHJD_ECOLI
Y147_MYCGE
DCE1_RAT
DCE1_RAT CVPR8 VGL1 ΩÏ DB

 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 0
 Length Query Match Score Result No.

P01810 mus musculu		Q9pht8 campylobact		_	P46558 caenorhabdi	P41149 mus musculu		Q99yk2 streptococc	P75585 mycoplasma		
HV40_MOUSE	CD63_BOVIN	TATC_CAMJE	AQP6_HUMAN	NADC_METJA	YKG8_CAEEL	MC5R_MOUSE	MC5R_RAT	MRAY_STRPY	Y147_MYCPN	Y432_MYCGE	Y432_MYCPN
, -1	Н	٦	Н	H	П	7	П	٦	Н	-	Н
119	236	245	282	283	317	325	325	336	377	398	404
•	٠	•	•	•	•	•	•	38.8	•	•	•
38	38	38	38	38	38	38	38	38	38	38	38
34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

012001. 012001. 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence updat 15-JUN-2002 (Rel. 41, Last annotation updat 10-JUN-2002 (Rel. 41, Last sequence updat 15-JUN-2002 (Rel. 41, Last sequence updat 15-JUN-2002 (Rel. 41, Last sequence updat 16.6 North of	ALG6_YI	EAST	K		ФФФ.		K		
01-809-1997 (Rel. 35, Created) 01-809-1997 (Rel. 35, Created) 01-809-1997 (Rel. 35, Last sequence update) 15-01W-2002 (Rel. 41, Last amnotation update) 2.4.1.7 (Dollogyl) 2.4.1.7 (Dollogyl) 2.4.2.7 (Rel. 40) 2.4.3 (Rel. 40) 2.4.4 (Rel. 40) 2.4.	T N	12001	STANDA	KD;	PKT;	244 1	AA.		
01-00V-1997 (Rel. 35 last sequence update) 15-JUN-2002 (Rel. 41. Last annotation update) D01(16)1 Proproposate Man9GlCRNAC alpha-1.3-glucosyltransferase (BC 2.4.1.) (D01Chyl-P-GLEMANGGLRNAC alpha-1.3-glucosyltransferase) D01(16)2 Proproposate Man9GlCRNAC alpha-1.3-glucosyltransferase) ALG6 OR YOROGAM ON UNAS4. Saccharomyces cerevisiae (Baker's yeast) Saccharomyces cerevisiae (Baker's yeast) Saccharomyces cerevisiae (Baker's yeast) Saccharomyces. MCB1_Tax1D-4932; SEQUENCE FROM N.A. WCB1_Tax1D-4932; SEQUENCE FROM N.A. WCB1_Tax1D-4932; SEQUENCE FROM N.A. WCB1_Tax1D-4932; SEQUENCE FROM N.A. WCB1_TAXID-4932; SECUENCE FROM N.A. WCB1_TAXID-4932; SECUENCE FROM N.A. WCB1_TAXID-4	i i	01-NOV-1997							
15-UN-2007 (Rel. 41, Last annotation update) Dolichly pyrophosphate MapGicNAc2-pp-dolichyl glucosyltransferase (EC 2.4.1) (DolichylCGIC:Man9GicNAc2-pp-dolichyl glucosyltransferase). ALGO OR YOROSA OR UNAS44. Saccharomyces cerevisiae (Baker's yeast). Bukaryota: Fungi; Ascomycota: Saccharomycotina; Saccharomycetes; Saccharomyces cerevisiae (Baker's yeast). Bukaryota: Fungi; Ascomycota: Saccharomycotina; Saccharomycetes; Saccharomyces cerevisiae (Baker's yeast). Saccharomyces cerevisiae (Baker's yeast). Saccharomyces of 30 kb fragment on the left arm of chromosome XV from Saccharomyces cerevisiae reveals 15 open reading frames, five of which correspond to previously identified genes."; SECHENCE FOR N.A. REDILNE-97051599; PubMed-8897369; REDILNE-9703144; PubMed-8877369; REDILNE-9704144; PubMed-8877369; REDILNE-9704144; PubMed-8877369; REDILNE-9704104 of the ALG6 locus of Saccharomyces cerevisiae required for glucose from full mthe N linked glycosylation of the ALG6 locus of Saccharomyces cerevisiae required for glucose from dolichyl phosphate glucose residue to the Lipid-linked oligosaccharide Man(9)GICNAC(2)-Pp-Dol	DI	01-NOV-1997		Last	nence	pdate	e)		
Dolichyl Prothosphate Man9GlcNAc2 alphà-1,3'glucosyltransferase (EC 2.4.1.7) (Dolichyl-D-CicramaglcNAc2-PP-dolichyl glucosyltransferase). ALG6 OR YORODW OR UNA54: Man9GlcNAc2-PP-dolichyl glucosyltransferase). BURATYCE: FUBJ; Ascomycota; Saccharomycotia; Saccharomycets; Saccharomycetales, Sacchar	DT	15-JUN-2002		Н	otation	pdn	ate)		
2.4.1.) (Dollorly1-P-Gl::Man9GlCNAC2-PP-dollorly1 glucosyltransferase). ALGG OR VORODZW OR UN5.44. Saccharomyces cerevisiae (Baker's yeast). EUKARTOTA FUNG1: Asconycota; Saccharomycottas; Saccharomycets; Saccharomyces cerevisiae (Baker's yeast). EUKARTOTA F. Hollorly1. SECHAROMY OR UNA. MEDLINE-9705159; PubMed-8895276; SECHAROMYCE FROW N.A. MEDLINE-9705159; PubMed-8895276; SECHAROMYCE FROW N.A. MEDLINE-9705159; PubMed-8897369; AMACTERIZATION. MEDLINE-970144; PubMed-8877369; REAST 12:1091-1095(1956). CHARACTERIZATION. CHARACTERIZATION. TISCHARACTERIZATION. TISCHARACTERIZATION. TISCHARACTERIZATION. CHARACTERIZATION. CHARACTERIZATION. TISCHARACTERIZATION. TIRCHARACTERIZATION. TISCHARACTERIZATION. TIRCHARACTERIZATION. THE STATISHARY: THANSARY TO ACTIVE SELONGS TO THE ALGE/ALGE GLUCOSTUTRANSFERASE FAMILY. THAN SENSEN-PROPER TO THE TY IS COPPYIGHT. THAN SENSEN-PROPER TO THE TY IS COPPYIGHT. THE STATISHARY: THAN SENSEN-PROPER ALGE AND THE ACT THE	DE	Dolichyl pyr	Sp	e Man9Gl	:NAc2 al	pha-	7)	yltransferase (EC	
ALGG OR YORONGY OR UNAS4. Saccharomyces cerevisiae (Baker's yeast). Eukaryota Fungi, Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycealses; Saccharomycetaceae; Saccharomyces. NNBLTWA.932; [1] SECURIKE FOON NA. WEDLINE—970319; Pubbed—8895276; Sterky F., Holmberg A., Pettersson B., Uhlen M.; The sequence of a 30 kb fragment on the left arm of chromosome XV from Saccharomyces cerevisiae reveals 15 open reading frames, five of which correspond to previously identified genes."; [1] RELY F., Holmberg A., Pettersson B., When M.; The sequence of a 30 kb fragment on the left arm of chromosome XV from Saccharomyces cerevisiae reveals 15 open reading frames, five of which correspond to previously identified genes."; [2] [2] RELY F., Holmberg A., Pettersson B., When M.; RELY F., Holmberg A., Pettersson B., When M.; RELY F., Holmberg A., Pettersson B., When M.; [2] RELY F., Holmberg A., Pettersson B., When M.; [3] RELY F., Holmberg A., Petterson B., Mobins P.W., Aebi M.; RELY F., Holmberg A., Petterson B., Rechard B., Aebi M.; RELY F., Holmberg A., Petterson B., A., Petterson B., Which Correspond to the M.; [4] RELY F., Holmberg A., A., Petterson B., Petterson B., A., Petterson B., Petterson B., Petterson B., A., Petterson B., A., Petterson B., Petterson	DE	2.4.1) (Do	ζŢ	Glc: Man 90	31cNAc2-	PP-dd		ucosyltransferase	
Saccharomycas carevisiae (Baker's yeast). Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomyces. [1] RNBLINE-9705159; Pubbed-8896276; Sterky F., Holmberg A., Pettersson B., Uhlan M.; SECURIC FROM N.A. MEDLINE-9705159; Pubbed-8896276; Sterky F., Holmberg A., Pettersson B., Uhlan M.; Tom Saccharomyces cerevisiae reveals 15 open reading frames, five of from Saccharomyces cerevisiae required for reast 12:1091-1095(1966). [2] CHARACTERIZATION MEDLINE-97031444; PubMed-8877369; Rabiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebl M.; Reliss G., te Heesen S., Zimmerman J., Robbins P.W., Aebl M.; Isolation of the ALG61 locus of Saccharomyces cerevisiae required for squooseylation in the N.linked glycosylation pathway."; Isolation of the ALG81 locus of Saccharomyces cerevisiae required for Jucose from dolichyl phosphate glucose (bol.P-GLO) onto the lipid-linked oligosaccharide precursor for N.linked glycosylation. I. FUNCTION: Adds the first glucose residue to the lipid-linked oligosaccharide precursor for N.linked glycosylation. I. FUNCTION: Adds the first glucose (bol.P-GLO) onto the lipid-linked oligosaccharide man (9)GlCNAC(2)-PP-Dol. I. PATHWAY: Glycosylation. I. SUBCELLUIAR LOCATION: Integral membrane protein. Endoplasmic retriculum (Fotential). I. SUBCELLUIAR LOCATION: Integral membrane protein is in no notified and this statement is one restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not remove and the European Bloinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no notified and this statement is not remove and an email to license@isb-sib.ch. EMBL: VARIOS: ALG6. ALG6. Transferase: Glycosyltransferase: Transmembrane; FRANSHEM 165 DOPERNIAGE. TRANSHEM 165 DOPER	GN	ALGE OR YORO	or Or	IA544.				ŧ	
Enkaryotai Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. NEDLINES-0432; [1] SEQUENCE FROW N.A. MEDLINES-0701599; PubMed-0896276; Sterky F., Holmberg A., Pettersson B., Uhlen M.; The sequence of a 30 kb fragment on the left arm of chromosome XV from Saccharomyces cerevisiae reveals 15 open reading frames, five of winch correspond to previously identified genes.; GHARATERIZATION. MEDLINES-0701444; PubMed-0807369; Reiss G., Te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; Isolation of the ALG6 lous of Saccharomyces cerevisiae required for glucosylation in the N-linked glycosylation pathway.", Glycoblody & 6493-498(1996). Ipid-10hx Adds the first glucose residue to the lipid-linked oligosaccharide Man(9)GLONAC(2)-PP-DOI. I- PURTION: Adds the first glucose residue to the lipid-linked oligosaccharide Man(9)GLONAC(2)-PP-DOI. I- FUNCTION: Adds the first glucose residue to the lipid-linked oligosaccharide Man(9)GLONAC(2)-PP-DOI. I- PURTHANY: GLYCOSYLON: Integral membrane protein. Endoplasmic reticulum (Potential). I- SUBCELLUIAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential). I- SUBCELLUIAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential). I- SUBCELLUIAR LOCATION: Integral membrane protein is in no nue by non-profit institutions as long as its content is no nue by non-profit institutions as long as its content is no entities requires a license agreement (See http://www.isb-slb.ch/announ or send an email to license@isb-sib.ch). ERBL: U4491: AAC4481.1; FRANSHEM 105 A39155: A196 A198. Fransferase; Glycosyltransferase; Transmembrane; FRANSHEM 36 Speciment 36 POTENTIAL. TRANSHEM 36 Speciment 36 POTENTIAL. TRANSHEM 36 Speciment 36 POTENTIAL. TRANSHEM 16 Speciment 37 POTENTIAL. TRANSHEM 16 Speciment 36 POTENTIAL.	SO	Saccharomyce	rev						
NCBI_TaxID=4932; Saccharomycetales; Saccharomycetaceae; Saccharomyces. NCBI_TaxID=4932; [1] SEQUENCE FROM N.A. MEDLINE=9705199; PubMed=8896276; SECTATE, T. Holmberg A., Pettersson B., Uhlen M.; The Sequence of a 30 kb fragment on the left arm of chromosome XV from Saccharomyces cerevisiae reveals 15 open reading frames, five of vast 12:1091-1096(1996). The Sequence of a 30 kb fragment on the left arm of chromosome XV from Saccharomyces cerevisiae reveals 15 open reading frames, five of vast 12:1091-1096(1996). CLARACTERIZATION. REDLINE=97031444; PubMed=887369; REDLINE=9703144; PubMed=887369; REDLINE=9703144; PubMed=887369; REDLINE=9703144; PubMed=887369; REDLINE=9703144; PubMed=887369; REDLINE=9703144; PubMed=887369; REDLINE=9703144; PubMed=887369; REDLINE=970314100; REMEL; VA4919; AAC494811; REMEL; VA4910; AAC494811; REMEL; VA	8	Eukaryota; F		comycota;	Sacchar	OMYC(charomycetes;	
VEBL_TaxID=4932; VEBL_TaxID=4932; VEBL_TaxID=4932; SEQUENCE FROM N.A. SEQUENCE OF a 30 kb fragment on the left arm of chromosome XV from secretaromyces cerevisiae reveals 15 open reading frames, five of which correspond to previously identified genes."; VEBLOADER 12:1091-1095(1996). VEBLOADER 12:1095(1996). VEBLOADER 13:1095(1996). V	ပ္ပ	Saccharomyce		ccharomy	etaceae	Sai		,	
SEQUENCE FROM N.A. MEDLINE-9705199; PubMed-8896276; SEQUENCE FROM N.A. MEDLINE-97051999; PubMed-8896276; Sterky F., Holmberg A., Pettersson B., Uhlen M.; The sequence of a 30 kb fragment on the left arm of chromosome XV which correspond to previously identified genes."; Yasat 12:1091-1095(1996). CHARACTERIZATION. CHARACTERIZATION. CHARACTERIZATION. Since the ALGG locus of Saccharomyces cerevisiae required for Glandston of the ALGG locus of Saccharomyces cerevisiae required for Insolation of the ALGG locus of Saccharomyces cerevisiae required for Glandstation in the N-linked glycosylation pathway."; CHARACTERIZATION. "Isolation of the ALGG locus of Saccharomyces cerevisiae required for Glycobiology 6:493-484 (1996). "Isolation in the N-linked glycosylation pathway."; Glycobiology 6:493-484 (1996).	XO	NCBI TaxID=4	•	7		•	•	·	
SEQUENCE FROM N.A. MEDLINE-97051599; PubMed-8896276; Steaky F., Hollmberg A., Pettersson B., Uhlen M.; Steaky F., Hollmberg A., Pettersson B., Uhlen M.; Steaky F., Hollmberg A., Pettersson B., Uhlen M.; from Saccharomyces cerevisiae reveals 15 open reading frames, five of which correspond to previously identified genes."; frast 12:1091-1095(1996). [2] [2] [3] [4] [5] [8] [8] [8] [8] [8] [8] [8] [8] [9] [9] [9] [1] [1] [1] [1] [1] [1] [1] [1] [1] [1	RN	[1]							
MEDLINE=97051599; PubMed-8896276; Sterky F., Holmberg A., Pettersson B., Uhlen M.; Sterky F., Holmberg A., Pettersson B., Uhlen M.; Factory. Holmberg A., Pettersson B., Uhlen M.; Factory. Holmberg A., Pettersson B., Uhlen M.; Factory. G. 30 kb fragment on the left arm of chromosome XV from Saccharomyces cerevisiae reveals 15 open reading frames, five of which correspond to previously identified genes."; Calman of the ALG6 locus of Saccharomyces cerevisiae required for GHARACTERIZATION. MEDLINE=97031444; PubMed-8877369; Rebbins P.W., Aebi M.; Rebss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; Rebline=97031444; PubMed-8877369; Resis G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; Reblino of the ALG6 locus of Saccharomyces cerevisiae required for glucosylation in the N.linked glycosylation pathway."; Glycobiology 6.493.498(1996)	70								
Sterky F., Holmberg A., Pettersson B., Uhlen M.; "The sequence of a 30 kb fragment on the left arm of chromosome XV from Saccharomyces cerevisiae reveals 15 open reading frames, five of which correspond to previously identified genes."; [2] [2] [2] [3] [4] [5] [6] [7] [8] [8] [8] [8] [8] [8] [8] [8] [9] [9] [9] [9] [9] [9] [9] [9] [9] [9	7 X C	MEDITNE=9705		Med=8896	.76.				
The sequence of a 30 kb fragment on the left arm of chromosome XV from Saccharomyces cerevisiae reveals 15 open reading frames, five of which correspond to previously identified genes."; Yeast 12:1091-1095(1996). CHARACTERIZATION. MEDINING-9703144; PubMed-8877369; Reiss G., te Heesen S., Zimmernan J., Robbins P.W., Aebi M.; Taolation of the ALG6 locus of Saccharomyces cerevisiae required for glucosylation of the N-linked glycosylation pathway."; CHARACTERIZATION. Reiss G., te Heesen S., Zimmernan J., Robbins P.W., Aebi M.; Reiss G., te Heesen S., Zimmernan J., Robbins P.W., Aebi M.; Reiss G., te Heesen S., Zimmernan J., Robbins P.W., Aebi M.; Reiss G., te Heesen S., Zimmernan J., Robbins P.W., Aebi M.; The N-linked glycosylation in the N-linked glycosylation arransfers glucose from Goligosaccharide Man(9)GlCNAC(2)-P-D-O).	40		,	Dotto	g 4000		2		
from Saccharomyces carevisuae reveals 15 open reading frames, five of vest 12:1091-1095(1996). [2] Anchre Correspond to previously identified genes."; [2] CHARCTERIZATION. [2] CHARCTERIZATION. [3] Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; [4] Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; [5] Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; [6] Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; [7] Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; [8] Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; [8] Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; [8] Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; [8] Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; [8] Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; [9] Clycobiology 6:493-498(1956). [1] FUNCTION: Adds the first glucose residue to the lipid-linked oligosaccharide precured membrane protein. Endoplasmic reticulum (Potential). [1] PATHWAY: Glycosylation: [1] Interventive Intervent in the Auge of Bioinformatics and the EMBL outstation on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commerce entities requires a license agreement (See http://www.isb-sib.ch/announ or sear in the Series Augement is not removed. [8] Rembl. 274910; CAA9910.1; [8] EMBL: U4391; AAC49481.1; [8] EMBL: ZA4910; CAA99190.1; [8] Fansferase: Glycosyltransferase: Transmembrane; Endoplasmic reticulum. [8] POTENTIAL. [8] POTENTIAL. [8] POTENTIAL. [8] POTENTIAL. [8] POTENTIAL.	\$ E	- 3	THIDET	1. V FELLE.	SSOIL B.	, of †	Len M.;	Omo omo a qu	
THOM SACCHARDING'S CEREVISIAGE TOWAGES 13 Open Leadung Itames, 1179 Of Veast 12:1091-1095(1996). [2] CHARACTERIZATION. [3] CHARACTERIZATION. MEDLINE-97031444; PubMed=8877369; Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; "Isolation of the ALG6 locus of Saccharomyces cerevisiae required for Glucosylation in the N-linked glycosylation pathway."; Glucosylation in the N-linked glycosylation pathway."; Glucosylation in the Precursor for N-linked glycosylation. Transfers of Jucose from dolichyl phosphate glucose (Dol-P-GLC) onto the lipid-linked oligosaccharide Man(9)GLONAC(2)-PP-DO1. -!- FUNCTION: Adds the first glucose (Dol-P-GLC) onto the lipid-linked oligosaccharide Man(9)GLONAC(2)-PP-DO1. -!- STUDELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential). -!- SINILARITY: BELONGS TO THE ALG6/ALG8 GLUCOSYLTRANSFERASE FAMILY. This SWISS-PROT entry is copyright. It is produced through a collaborat between the Swiss Institute of Bioinformatics and the EMBL outstation would file and this statement is not removed. Usage by and for commerce that European Bioinformatics Institute. There are no restrictions on use by non-Profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commerce thities requires a license alreement (See http://www.isb-sib.ch/announ or send an email to license alreement (See http://www.isb-sib.ch/announ or send an email to license alreement (See http://www.isb-sib.ch/announ or send an email to license alreement (See http://www.isb-sib.ch/announ or send an email to license alreement (See http://www.isb-sib.ch/announ or send an email to license alreement (See http://www.isb-sib.ch/ansferase; Transmembrane; Endoplasmic reticulum. Transferase; Glycosylltransferase; Transmembrane; Endoplasmic reticulum. TRANSMEM 105 55 Alg6_Alg8 1. TRANSMEM 105 500055250 Alg6. TRANSMEM 105 500055250	I E	onanhas ant	ָר ב בי	ND II ay	וופוזר טוו	י נוני	בין בין	CILLUMOSOME AV	4
Which correspond to previously toentified genes.; Yeast 12:1091-1095(1996). CHARACTERIZATION. MEDLINE=97031444; PubMed-8877369; Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; Glycoslation in the N-linked glycosylation. Transfers Glycosylation.	K.I.	•	ა გე 1	revisiae	reveals	CT	open	rames, tive	4
Teast 12:1091-1095(1996). [2] CHARACTERIZATION. MEDLINE=97031444; PubMed=8877369; Reiss G., te Heesen S., Zimmernan J., Robbins P.W., Aebi M.; Reiss G., te Heesen S., Zimmernan J., Robbins P.W., Aebi M.; Reiss G., te Heesen S., Zimmernan J., Robbins P.W., Aebi M.; Reiss G., te Heesen S., Zimmernan J., Robbins P.W., Aebi M.; Reiss G., te Heesen S., Zimmernan J., Robbins P.W., Aebi M.; [1] Reiss G., te Heesen S., Zimmernan J., Robbins P.W., Aebi M.; [2] Reiss G., te Heesen S., Zimmernan J., Robbins P.W., Aebi M.; [3] Reiss G., te Heesen S., Zimmernan J., Robbins P.W., Aebi M.; [3] Reiss G., te Heesen S., Zimmernan J., Robbins P.W., Aebi M.; [4] Risobiology 6,493-498(196). [5] Reiss G., te Heesen S., Zimmernan Lebender Dipid-linked Gliphy Phosphate glucose (Dol-P-GLC) onto the Lipid-linked oligosaccharide Man(9)GloNAc(2)-PP-DGl. onto the Lipid-linked oligosaccharide Man(9)GloNAc(2)-PP-DGl. [6] Reiss G., te Heesen S., Robbins G., Robbins M., Reiss G., Robetween the Swiss Institute of Bioinformatics and the Emple onto Profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch). [EMBL; Z74910; CAA99190.1; EMBL; U43491; AAC49481.1; EMBL; U43491; AAC494	KI.	which corres	ָי ט	reviousi	.denti	rred			
CHARCTERIZATION. MEDLINE=9703144; PubMed=8877369; Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; "Isolation of the ALG6 locus of Saccharomyces cerevisiae required for glucosylation in the N-linked glycosylation pathway."; Glycobiology 6.493-498(1996). -! FUNCTION: Adds the first glucose residue to the lipid-linked oligosaccharide precursor for N-linked glycosylation. Transfers glucose from dolichyl phosphate glucose (Dol-P-GLC) onto the lipid-linked oligosaccharide Man(9)GlCNAC(2)-PP-Dol. -!- STATUMAR: Glycosylation. -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential). -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential). -!- SIMILARITY: BELOMGS TO THE ALG6/ALG8 GLUCOSYLTRANSFERASE FAMILY. This SWISS-PROT entry is copyright. It is produced through a collaborat between the Swiss Institute of Bioinformatics and the EMBL outstation on see by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch). EMBL: U43491; AAC49481.1; EMBL: U43491; AAC49481.1	RL.	Yeast 12:109	ζ.	. (96)					
CHARACTERIZATION CHARACTERIZATION CHARACTERIZATION CHARACTERIZATION Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; "Isolation of the ALG6 locus of Saccharomyces cerevisiae required for glucosylation bathway."; Glycobiology 6:493-498 (1996) -!- FUNCTION: Adds the first glucose residue to the lipid-linked oligosaccharide precursor for N-linked glycosylation. Transfers glucose from dolichyl phosphate glucose (Dol-P-GLC) onto the lipid-linked oligosaccharide Man (9)GLOROC(2)-PP-DOI!- PATHWAY: Glycosylation!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential)!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential)!- SIMILARITY: BELONGS TO THE ALG6/ALG8 GLUCOSYLTRANSFERASE FAMILY. This SWISS-PROT entry is copyright. It is produced through a collaborat between the Swiss Institute of Bioinformatics and the EMBL outstatio as long as its content is in no modified and this statement is not removed. Usage by and for commercentiies requires a license agreement (See http://www.isb-sib.ch/announ or send an enail to license@isb-sib.ch)	Z I	[7]	;						
MEDLINE-9701144; PubMed-8877369; MEDLINE-97011444; PubMed-8877369; Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; "Isolation of the ALG6 locus of Saccharomyces cerevisiae required for glucosylation in the N-linked glycosylation pathway."; Glycobiology 6:493-498 (1996)!- FUNCTION: Adds the first glucose residue to the lipid-linked oligosaccharide precursor for N-linked glycosylation. Transfers glucose from dolichyl phosphate glucose (Dol-P-Glc) onto the lipid-linked oligosaccharide Man (9)GlcNac(2)-PP-Dol!- SUMCLECHOLNE LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential)!- SIMILARITY: BELOGS TO THE ALG6/ALG8 GLUCOSYLTRANSFERASE FAMILY!- SIMILARITY: BELOGS TO THE ALG6/ALG8 GLUCOSYLTRANSFERASE FAMILY. This SWISS-PROT entry is copyright. It is produced through a collaborat between the Swiss Institute of Bloinformatics and the EMBL outstations on use by non-profit institutions as long as its content is in no use by non-profit institutions as long as its content is in no use by non-profit institutions as long as large by and for commercenties requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch). EMBL; U43491; AAC49481.1; EMBL; U43491; AAC49481.1; EMBL; U43491; AAC49481.1; EMBL; TA4910; CAA99190.1; EMBL; TAANSMEM 105 Alg6_Alg8. TRANSMEM 105 TATANSMEM 105 POTENTIAL. TRANSMEM 106 TATANSMEM 106 POTENTIAL.	RP	CHARACTERIZA	TION.		1				
Reiss G., te Heesen S., Zimmerman J., Robbins P.W., Aebi M.; "Isolation of the ALG6 locus of Saccharomyces cerevisiae required for glucosylation in the N-linked glycosylation pathway."; glucosylation in the N-linked glycosylation pathway."; glucosylation. Adds the first glucose residue to the lipid-linked oligosaccharide precursor for N-linked glycosylation. Transfers glucose from dolichyl phosphate glucose (Dol-P-G1C) onto the lipid-linked oligosaccharide Man(9)GlcNac(2)-PP-Dol	RX	=9703	44;	Med=8877.	369;				
"Isolation of the ALG6 locus of Saccharomyces cerevisiae required for glucosylation in the N-linked glycosylation pathway."; Glycobiology 6:493-498(1996). -!- FUNCTION: Adds the first glucose residue to the lipid-linked oligosaccharide precursor for N-linked glycosylation. Transfers glucose from dolichly phosphate glucose (Dol-P-GlC) onto the lipid-linked oligosaccharide Man(9)GlCNAC(2)-PP-Dol. -!- PATHWAY: Glycosylation!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential)!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential)!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential)!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic meticulum (Potential)!- SUBCELLULAR LOCATION: Integral membrane is produced through a collaborat between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commerce entities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@ilb-sib.ch/). EMBL; U44910; CAA99190.1; EMBL; U44910; CAA99190.1; EMBL; 274910; CAA99190.1; EMBL; 274910; CAA99190.1; EMBL; 274910; CAA99190.1; EMBL; 274910; CAA99180.1; EMBL; 274910; CAA99180.1; EMBL; 274910; CAA99190.1; EMBL; 274910; CAA991190.1; EMBL; 274910; CAA99190.1; EMBL; 274910; CAA991	RA		leese	., Zimme	man J.,	Rob	bins P.W.,	., . Σ	
glucosylation in the N-linked glycosylation pathway."; Glycoblology 6:493-498(996)!-FUNCTON: Adds the first glucose residue to the lipid-linked oligosaccharide precursor for N-linked glycosylation. Transfers glucose from dolichyl phosphate glucose (Dol-P-GlC) onto the lipid-linked oligosaccharide Man(9)GlCNAC(2)-PP-Dol!- PATHWAY: Glycosylation: Integral membrane protein. Endoplasmic reticulum (Potential)!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential)!- SIMILARITY: BELONGS TO THE ALG6/ALG8 GLUCOSYLTRANSFERASE FAMILY!- SIMILARITY: BELONGS TO THE ALG6/ALG8 GLUCOSYLTRANSFERASE FAMILY!- SIMILARITY: BELONGS TO THE ALG6/ALG8 GLUCOSYLTRANSFERASE FAMILY!- SIMILARITY: BELONGS TO THE ALG6/ALG8 GLUCOSYLTRANSFERASE FAMILY This SWISS-PROT entry is copyright. It is produced through a collaborat between the Swiss Institute of Bioinformatics and the EMBL outstations on use by non-profit institutions as long as its content is in no use by non-profit institutions as long as its content is in one entities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch) EMBL; 744910; CAA99190.1; SGD; SO006528; ALG6 InterPro; IPR004856; Alg6_Alg8 FARANSMEM 105 L25 POTENTIAL TRANSMEM 105 L25 POTENTIAL TRANSMEM 106 L26	RT		the	6 locus	of Sacch	arom	yces cerev	required	'n
Glycobiology 6:493-498(1996). -!- FUNCTION: Adds the first glucose residue to the lipid-linked oligosaccharide precursor for N-linked glycosylation. Transfers glucose from dolichyl phosphate glucose (Dol-P-Glc) onto the lipid-linked oligosaccharide Man(9)GlCNAC(2)-PP-Dol!- PATHWAY: Glycosylation!- SUBCELLUIAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential)!- SIMILARITY: BELONGS TO THE ALG6/ALG8 GLUCOSYLTRANSFERASE FAMILY!- SIMILARITY: BELONGS TO THE ALG6/ALG8 GLUCOSYLTRANSFERASE FAMILY. This SWISS-PROT entry is copyright. It is produced through a collaborat between the Swiss Institute of Bioinformatics and the EWBL outstations on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch). EWBL: 774910; CAA99190.1; - SGD; SO005528; ALG6. InterPro; IPR004856, Alg6_Alg8; 1. Transferase: Glycosyltransferase; Transmembrane; Endoplasmic reticulum. TRANSMEM 105 125 POTENTIAL. TRANSMEM 106 125 POTENTIAL. TRANSMEM 106 126	RT	$\overline{}$	in t	N-linked	glycosy	lati	on pathway		
-!- FUNCTION: Adds the first glucose residue to the lipid-linked oligosaccharide precursor for N-linked glycosylation. Transfers glucose from dolichyl phosphate glucose (Dol-P-GLC) onto the lipid-linked oligosaccharide Man(9)GLONAC(2)-PP-DOL!- PATHWAY: Glycosylation!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential)!- SIMILARITY: BELONGS TO THE ALG6/ALG8 GLUCOSYLTRANSFERASE FAMILY!- SIMILARITY: BELONGS TO THE ALG6/ALG8 GLUCOSYLTRANSMEM 16 The ALG6/ALG8 GLUCOSYLTRANSMEM 16 The ALG6/ALG8 GLUCOSYLTRANSMEM 16 TRANSMEM 16 TRAN	RL	_	:493	18(1996).	•		1		
oligosaccharide precursor for N-linked glycosylation. Transfers glucose from dolichyl phosphate glucose (Dol-P-Glc) onto the lipid-linked oligosaccharide Man(9)GlcNAc(2)-PP-Dol.	ည		Adds	e first	llucose	resi	due to the	lipid-linked	
glucose from dolichyl phosphate glucose (Dol-P-GlC) onto the lipid-linked oligosaccharide Man(9)GlcNAc(2)-PP-Dol.	ပ္ပ	oligosac	arid	recursor	for N-1	inke	d glycosyl	ation. Transfers	
lipid-linked oligosaccharide Man(9)GlcNAc(2)-PP-Dol.	ပ္ပ	qlucose	Q	chyl pho	sphate q	luco	se (Dol-P-	Glc) onto the	
-!- PATHWAY: Glycosylation!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential)!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential)!- SIMILARITY: BELONGS TO THE ALG6/ALG8 GLUCOSYLTRANSFERASE FAMILY!- SIMILARITY: BELONGS TO THE ALG6/ALG8 GLUCOSYLTRANSFERASE FAMILY. This SWISS-PROT entry is copyright. It is produced through a collaborat between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch). EMBL; U43491; AAC49481.1; EMBL; U43491; AAC494856; Alg6_Alg8	ည	lipid-li	O	rosacchar	de Man(9)61	cNAc(2)-PP	-Doi.	
-:- SUBCELLULLAR LOCATION: Integral membrane protein. Endoplasmic reticulum (Potential):- SIMILARITY: BELONGS TO THE ALG6/ALG8 GLUCOSYLTRANSFERASE FAMILY:- SIMILARITY: BELONGS TO THE ALG6/ALG8 GLUCOSYLTRANSFERASE FAMILY. This SWISS-PROT entry is copyright. It is produced through a collaborat between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercenties requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch). EMBL; U43491; AAC49481.1; EMBL; U43491; A	ည	! - PATHWAY:	Ö	ation.					
reticulum (Potential). -!- SIMILARITY: BELONGS TO THE ALG6/ALG8 GLUCOSYLTRANSFERASE FAMILY. This SWISS-PROT entry is copyright. It is produced through a collaborat between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch). EMBL, U43491; AAC49481.1; - EMBL, U43491; AAC49481.1; - EMBL, S74910; CAA99190.1; - EMBL, S74910; CAA99190.1; - EMBL, S74910; CAA9918.1 Transferase; Glycosyltransferase; Transmembrane; Endoplasmic reticulum. TRANSMEM 105 125 POTENTIAL. TRANSMEM 106 166 POTENTIAL.	ຍ	! - SUBCELLU	Q	ION: Inte	egral me	mbra	ne protein	. Endoplasmic	
This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commerce entities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch). EMBL; U43491; AAC49481.1;	ນ	reticulm	Pot	ial).	1		4	•	
This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commerce entities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch). EMBL; U43491; AAC49481.1;	2	1	BF	IGS TO THE	3 ALG6/A	1.68	GLUCOSYLTR	ANSFERASE FAMILY.	
This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch). EMBL; U43491; AAC49481.1;		. ;	1 1			1			
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch). EMBL; U43491; AAC49481.1; EMBL; Z74910; CAA99190.1; EMBL; Z74910;			e u		right. I	+ 18	nced	through a collabo	ration
the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch). EMBL; U43491; AAC49481.1; EMBL; U43491; AAC49491.1; EMBL; U43491; AAC49491.	2	đ	C.	stitute (of Bioin	form	stics and	the EMBI outsta	tion -
use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch). EMBL; U43491; AAC49481.1; EMBL; Z74910; CAA99190.1; SGD; S0005528; ALG6. InterPro; IPR004856; Alg6_Alg8. Fransferase; Glycosyltransferase; Transmembrane; Endoplasmic reticulum. TRANSMEM 105 125 POTENTIAL. TRANSMEM 105 125 POTENTIAL. TRANSMEM 146 166		Furon	Bioin	matics	stitute		here are n	o restrictions o)
modified and this stentities requires a or send an email to	20	nou Aq	-profit	institut	ons as	long	as its c	ontent is in n	NA WAY
entities requires a or send an email to	S C	ified and	this si	tement is	not re	move.	d. Usage	by and for comm	ercial
or send an email to		S	(0	icense a	reement	(Se	e http://w	ww.isb-sib.ch/ann	onuce/
EMBL; U43491; AAC494 EMBL; Z74910; CAA997 SGD; S0005528; ALG6 InterPro; IPR004856 Pfam; PF03155; Alg6- Transferase; Glycosy Endoplasmic reticuly TRANSMEM 36 TRANSMEM 105	ນ	r send a	to	icense@i	b-sib.c	h).			
EMBL; U43491; AAC499 EMBL; Z74910; CAA999 SGD; S0005528; ALG6 InterPro; IPR004856 Pfam; PF03155; Alg6 Transferase; Glycosy Endoplasmic reticuly TRANSMEM 36 TRANSMEM 105	S		1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1	1 1 1 1 1 1 1 1 1		
EMBL; Z74910; CAA99190.1; SGD; S0005528; ALG6. InterPro; IPR004856; Alg6_Alg8. Pfam; PF03155; Alg6_Alg8; 1. Transferase; Glycosyltransferase; Endoplasmic reticulum. TRANSMEM 36 56 POTENTRANSMEM 105 125 POTENTRANSMEM 146 166	DR	U43	149	11.1;					
SGD; S0005528; ALG6. InterPro; IPR004856; Alg6_Alg8. Pfam; PF03155; Alg6_Alg8; 1. Transferase; Glycosyltransferase; Endoplasmic reticulum. TRANSMEM 36 56 POTEN TRANSMEM 105 125 POTEN	DR	2749	CAA9	.1;					
InterPro; IPR004856; Alg6_Alg8. Pfam; PF03155; Alg6_Alg8; 1. Transferase; Glycosyltransferase; Endoplasmic reticulum. TRANSMEM 36 56 POTEN TRANSMEM 105 125 POTEN TRANSMEM 146 166 POTEN	DR	000	ALG						
Pfam; PF03155; Alg6_Alg8; 1. Transferase; Glycosyltransferase; Endoplasmic reticulum. TRANSMEM 36 56 POTEN TRANSMEM 105 125 POTEN TRANSMEM 146 166 POTEN	DR	0	0485	Alq6_Alq	٠.				
Transferase; Glycosyltransferase; Endoplasmic reticulum. TRANSMEM 36 56 POTEN TRANSMEM 105 125 POTEN	DR	PF03	Alq	11q8; 1.					
Endoplasmic reticulum. TRANSMEM 36 56 POTEN TRANSMEM 105 125 POTEN TRANSMEM 146 166 POTEN	ΚW	eras	Lvco	transfer	se:	nsme	mbrane;		
TRANSMEM 36 56 TRANSMEM 105 125 TRANSMEM 146 166	KW	ic	ticu	ٔ			•		
TRANSMEM 105 125 TRANSMEM 146 166	T.T.) 	1		AT TRNT TA	- -			
TRANSMEM 146 166	FT		05		OTENTIA	Ĥ.			
	FT		46		OTENTIA			•	

16

CGIDFILFWIFW

S

δ

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s in no way
for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL outstation trictions on it
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ronavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIRUS MORPHOGENESIS AND MAY BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AYER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IAL)
                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=93057357; PubMed=1431811;
Horsburgh B.C., Brierley I., Brown T.D.K.;
Horsburgh B.C., Brierley I., Brown T.D.K.;
"Analysis of a 9.6 kb sequence from the 3' end of canine corgenomic RNA.";
J. Gen. Virol. 73:2849-2862(1992).

-!- FUNCTION: TARGETS THE SITE OF VIRUS MORPHOGENESIS AND MP IMPLICATED IN VIRAL PATHOGENESIS.

-!- SUBCELLULAR LOCATION: LARGELY EMBEDDED IN THE LIPID BILF
-!- SUBCELLULAR LOCATION: LARGELY EMBEDDED IN PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMI the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sior send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENT)
O-LINKED (POTENTIAL).
O-LINKED (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENT)
35C6D45DC6A474F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            Canine enteric coronavirus (strain Insavc-1) (CCV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidov
Coronaviridae; Coronavirus.
NCBI_TaxID=36391;
                                                                                                                                                Length 544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 262;
                                                                                                                                                                                                                                                                                                                (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
tein precursor (Matrix glycoprotein) (Membrane
                                                                                                                                                                          Indels
                                                                                                                      64BFA11A1F6D02B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Signal
                                                                                                                                                                           4;
                                                                                                                                                 ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E1 GLYCOPROTEIN POTENTIAL.
                                                                                                                                               Score 50; DB 1
Pred. No. 1.3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48; DB Pred. No. 1.4;
                           POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL. POTENTIAL.
                                                      POTENTIAL. POTENTIAL.
                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                POTENTIAL
                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JO1724; JO1724.
JO1724; JO1724.

PPO1635; Corona_M; 1.

Tx protein; Transmembrane; G
                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262
72 P
101
134 P
32
33
60
44
55
N
29508 MW;
                                                                                                                    62782 MW;
                                                                                                                                                51.0%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.0%;
                                                                                                                                                                                                                           514 NCAVGFICFSIFW 526
                                                                                                                                                                                                                                                                                                                                                         glycoprotein precursor
                                                                                                                                                                                                 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D13096; BAA02413.1;
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                          STANDARD;
  192
244
284
353
377
419
416
502
529
                                                                                                                                                                                                  NCGIDFILFWLFW
                                                                                                                                            uery Matcn
est Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1
18
56
85
115
32
33
44
55
                                                                                                                      AA;
172
224
224
333
357
357
426
482
5482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matrix protein; SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                       glycoprotein)
                                                                                                                                                                                                                                                                                                                  01-JUN-1994
01-JUN-1994
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JQ1724;
                                                                                                                                                                                                                                                                                          VME1_CVCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                     P36299;
                                                                                                                                                                                                                                                                CVCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                       Matches
                                                                                                                                                            Best
                                                                                                                                                                                                                                                                ULT
                                                                                                                                                                                                                           a
d
                                                                                                                                                                                                                                                                                                                              DT DT DT OC OC OC OC
                                       FT
FT
FT
SO
                                                                                                                                                                                                 ð
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Sprague-Dawley; TISSUE=Aorta;

MEDLINE=90222168; PubMed=2109324;

Ross P.C., Figler R.A., Corjay M.H., Barber C.M., Adam N.,

Harcus D.R., Lynch K.R.;

"RTA, a candidate G protein-coupled receptor: cloning, sequencing,

and tissue distribution.";

Proc. Natl. Acad. Sci. U.S.A. 87:3052-3056(1990).

-!- FUNCTION: ORPHAN RECEPTOR.

-!- FUNCTION
                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M35297; AAA42087.1; -.
EMBL; M35298; AAA42088.1; -.
PIR; A35639; A35639.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 1 44 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LINKED (GLCNAC. . .) (
E4630007770941F4 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                    01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
Probable G protein-coupled receptor RTA.
RTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 45; DB
Pred. No. 5.2;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 (POTENTIAL).
CYTOPLASMIC (P
N-LINKED (GLCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38364 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.9%;
                    92
                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | | | : | |: | CGIKMLIMMLLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                             RESULT
                                                                                                                                                                                                                                                                                                           DT
```

ö

Gaps

; 0

Indels

1;

3;

Conservative

Similarity 6; Conser

ö

Gaps

ö

Indels

4;

Mismatches

ä

Conservative

9

Similarity

Local

Best Loc Matches

```
Zheng L.,
Smith H.O.,
                                                                                                                                                                                                       н
Н
                                                                                                                                                                                                                                                         c.,
etchum K.A.
                                                                                                                                                                                                                                                                                                                                                                                                       in the
                                                                                          Hexapoda;
                                                                                  Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapo Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                               Dunipace L., Meister S., McNealy C., Amrein H.; "Spatially restricted expression of candidate taste receptors Drosophila gustatory system."; Curr. Biol. 11:822-835(2001).
                                                                 update)
                                         406 AA
                                                            update,
                                        G64B_DROME STANDARD; PRT; 4
P83294; Q9VZJ7;
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
15-JUN-2002 (Rel. 41, Last annotation
Putative gustatory receptor 64b.
GR64B OR CG14986.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Robertson H.;
Unpublished observations (NOV-2001)
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21407712; PubMed=11516643;
            265
15
                                                                                                                                                                                                                                                                                                                                                                                                                               CONCEPTUAL TRANSLATION
GIDFIIFWIF
      |||: :||:|
GIDWFLFWVF
                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION
9
           256
                                                     TO
TO
                                                                       d
ŏ
```

P.,

. ∡

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                 erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=Mu50 / ATCC 700699, and N315;
MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shibe
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
aureus.";
                  protein (Potential)
G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                             coupled receptor;
                                                            CAUTION: Ref.1 sequence differs from that shown due to gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                     1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                         EMBL; AE003480; AAF47824.1; ALT_SEQ.
FlyBase; FBgn0045478; Gr64b.
Hypothetical protein; Receptor; G-protein coupled recel
Transmembrane; Glycoprotein; Multigene family.
DOMAIN
1 47 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         occus aureus (strain Mu50 / ATCC 700699), and occus aureus (strain N315). Firmicutes; Bacillales; Staphylococcus. >=158878, 158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F6A37DD9E1E58B88 CRC64;
FUNCTION: Probable role in the gustatory response
SUBCELLULAR LOCATION: Integral membrane protein (1
SIMILARITY: BELONGS TO FAMILY DR-TR OF G-PROTEIN (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45; DB 1;
Pred. No. 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARAB_STAAM STANDARD; PRT; 545 AA. 099W57; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) L-ribulokinase (EC 2.7.1.16). ARAB OR SAV0552 OR SA0510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ж
Э
                                                                                                                                                                                                                                                                                                  SUBFAMILY II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 NCGIDFIIFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | |:||:: ||
291 NIGVDFLVMLAFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aure
Bacteria; Firmicute
NCBL_TaxID=158878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                       448
69
1131
1152
1152
1152
2055
3371
3371
355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus
                                               RECEPTORS.
                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STAAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                             ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARAB_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DT
DE
GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    덥
```

ö

H

Shiba

aureus."; Lancet 357:1225-1240(2001)

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ol-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sucrose synthase (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. Columbia;
MEDLINE=92119221; PubMed=1531031;
Chopra S., Del-Favero J., Dolferus R., Jacobs M.;
Chopra S., Del-Favero J., Dolferus R., Jacobs M.;
"Sucrose synthase of Arabidopsis: genomic cloning and sequence characterization.";
Plant Mol. Biol. 18:131-134(1992).
-!- FUNCTION: SUCROSE-CLEAVING ENZYME THAT PROVIDES UDP-GLUCOSE AND FRUCTOSE FOR VARIOUS METABOLIC PATHWAYS.
-!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.
-!- INDUCTION: BY ANAEROBIC STRESS.
-!- INDUCTION: BY ANAEROBIC STRESS.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1. PLANT SUCROSE SYNTHASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
 5-
                                                                                                                                                                                                                                                                                                                                                                                                         Φ
                                                                                                                                                                                                                                                                              EMBL; AP003359; BAB56714.1; -.
EMBL; AP003130; BAB41741.1; -.
InterPro; IPR000577; FGGY_kin.
Pfam; PF00370; FGGY, 1.
Pfam; PF02782; FGGY_C; 1.
Transferase; Kinase; Arabinose catabolism; Complete proteoms SEQUENCE 545 AA; 60965 MW; E3917036237CEA4B CRC64;
   + L-ribulose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001296; Glycos_transf_1.
InterPro; IPR000368; Sucrose_synth.
Pfam; PF00534; Glycos_transf_1; 1.
Pfam; PF00862; Sucrose_synth; 1.
Transferase; Glycosyltransferase; Multigene family
                                  FAITHWAY: L-arabinose catabolism; second step.
SIMILARITY: BELONGS TO THE RIBULOKINASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ж
;
   ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB Pred. No. 16; 3; Mismatches
  + L-ribulose
 CATALYTIC ACTIVITY: ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::|||: | ||
195 RSNCGLGFKAFW 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X60987; CAA43303.1;
S19125; YUMU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QANCGIDFIIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUS2_ARATH
Q00917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUS2_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RA
RT
RL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.
                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                         ô
                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hypothetical 17.3 kDa protein in SEC15-SAP4 intergenic region.
YGL230C.
                            Length 804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 147
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                        Fartmann B., Kramer B., Kramer W.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
F8F040A1D618CD96 CRC64;
3E727D3CDFF9A4B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AF2131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ore 42; DB 1 ed. No. 7.2; Mismatches
                                                                                                                                                                                            147 AA
                             DΒ
                           Score 43; DB Pred. No. 23;
                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 272752; CAA96948.1; -. SGD; S0003199; YGL230C. Hypothetical protein; Transmembrane TRANSMEM 85 105 POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17262 MW;
91989 MW;
                            43.9%; 62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.9%;
larity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAIOFLFFIIYW 107
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 CGIDFIIFWIFW 16
                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaeoglobus fulgidus
                                                                                      16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 6; Conserv
                                           Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 AA;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE FROM N.A.
                                                                                                                    19 FLSFWVFW
                                                                                      9 FILFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YL31_ARCFU
ID YL31_ARCFU
AC 028149;
                                                                                                                                                                                          YGY0_YEAST
P53074;
SEQUENCE
                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                 SULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best
                                                                                                                                                              RESULT
YGYO_
                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QY
```

```
a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                sib.ch/announce,
                                                                                                                                                                                                                                     commercia
                                                                                                                                                                            There are no restrictions on it ed. Usan
                 Zhou L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lowe J.B.;
n lymphoid
ion of L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith P.L., Gersten K.M., Petryniak B., Kelly R.J., Rogers C.,
Natsuka Y., Alford J.A. III, Scheidegger E.P., Natsuka S., Lowe J.
"Expression of the alpha(1,3)fucosyltransferase Fuc-TVII in lympho aggregate high endothelial venules correlates with expression of I selectin ligands.";
J. Biol. Chem. 271:8250-8259(1996).
-!- FUNCTION: MAY CATALYSE ALPHA-1,3 GLYCOSIDIC LINKAGES INVOLVED THE EXPRESSION OF SIALYL LEWIS X ANTIGENS.
-!- CATALYTIC ACTIVITY: GDP-L-fucose + alpha-2,3-Neu-N-acetyl-1,4-beta-D-galactosyl-P-galactosyl-Galactosyl-(alpha-1,3-L-fucosyl)-N-acetyl-1,4-beta-D-galactosyl-(alpha-1,3-L-fucosyl)-N-acetyl-D-glucosaminyl-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                     lphate
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus F Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zh Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                    "The complete genome sequence of the hyperthermophilic, sulphate reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMB the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content imposified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-silor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Galactoside (FUCT-VII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                        Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C07CAFD427DC26F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alpha-(1,3)-fucosyltransferase (EC 2.4.1.-) (fucosyltransferase) (Fucosyltransferase 7) (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
S
                                                                                                                                                                                                                                                                                                                      Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=NIH Swiss;
MEDLINE=96215226; PubMed=8626519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,;
;;
                                                                                                                                                                                                                                                                                                                                 24
56
114
146
181
218
253
285
328
37066 MW;
                                                                                         omplete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.48;
                                                                                                                                                                                                                                                                                      EMBL; AE000957; AAB89128.1
TIGR; AF2131; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                    Hypothetical protein;
TRANSMEM 5 2
TRANSMEM 34 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
tes 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N:A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 IIFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILFWLFW
                                                                                                                                                                                                                                                                                                                                                34
124
124
159
196
231
263
306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUT7_MOUSE
Q11131;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304
                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUT7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 달
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
```

```
is produced through a collaboration ormatics and the EMBL outstation -
                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
MPTPCPPACLSTPGTHRLLPFPDWKAPSWESRKEATCNSSS
MPTPCPPACLSTPGTHRLLPFPDWKAPSWESRKEATCNSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                               Glyco_transf_10; 1.

Glycosyltransferase; Transmembrane; Glycoprotein;

Glycosyltransferase; Transmembrane; Glycoprotein;

Golgi stack; Alternative splicing.

CYTOPLASMIC (POTENTIAL).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                  AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                  MARROW AN
                  MEMBRANE-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lascn11.";
snce 273:1058-1073(1996).
SUBCELLULAR LOCATION: Integral membrane protein (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                  10
                                                  ..
?:
                                                                                  GLAND BONE
                                                                                                                                  SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY
                                                 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methanococci; Methanococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                              ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG AND TO A MUCH LESSER EXTENT IN SPLEEN, SALIVARY GLANI
                 II MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        342 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ed. No. 17;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanocaldococcaceae; Methanocaldococcus
NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                   GOLGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred
PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: TYPE
FORM IN TRANS CISTERNAE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44494 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein MJ0762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5%;
                                                                                                                                                                                                                                                                                                                                                  GT_10
                                                                                                                                                                                                                                                                                               EMBL; U45980; AAC52484.1;
EMBL; U45980; AAC52485.1;
MGD; MGI:107692; Fut7.
InterPro; IPR001503; GT_10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIDFIIFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389
128
338
51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATFMVIWFFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79
128
338
                                                                                                                                                                                                                                                                                                                                                                   PF00852;
                                                                                                                                                                                                                                                                                                                                                                                                    Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                   Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997
01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y762_METJA
Q58172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89
                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best
qq
```

```
fh a collaboration
EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a collaboration
                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
Marchantiopsida; Marchantiidae; Marchantiales; Marchantiineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of
       S. POMBE MALATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     verwort
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fukuzawa H., Ohyama K.; "Cotranscriptional expression of mitochondrial genes for subunits "Cotranscriptional expression of mitochondrial genes for subunits NADH dehydrogenase, nad5, nad4, nad2, in Marchantia polymorpha."; Mol. Gen. Genet. 237:343-350(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , N 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                К.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oda K., Yamato K., Ohta E., Nakamura Y., Takemura M., Nozat, Akashi K., Kanegae T., Ogura Y., Kohchi T., Ohyama K.; "Gene organization deduced from the complete sequence of limarchantia polymorpha mitochondrial DNA. A primitive form o mitochondrial genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                           Transport; Complete pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamato K., Ohta E., Takemura M., Akashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08EFEC3E2C4955D8 CRC64;
 SIMILARITY: STRONG, TO M.JANNASCHII MJ0576 AND TO PERMEASE (MAE1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Last annotation update)
NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ore 41; DB ed. No. 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                              erPro; IPR004695; C4dic_mal_transp.

1; PF03595; C4dic_mal_tran; 1.

EAMS; TIGR00816; tdt; 1.

thetical protein; Transmembrane; Transmem 8 28 POTENTIAL.

SMEM 39 59 POTENTIAL.

MEM 108 128 POTENTIAL.

MEM 142 162 POTENTIAL.

MEM 207 227 POTENTIAL.

MEM 207 227 POTENTIAL.

MEM 242 262 POTENTIAL.

MEM 324 324

CE 342 AA; 2262

CE 342 AA; 2262

CE 342 AA; 2262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1992 (Rel. 23, Created)
01-FEB-1994 (Rel. 28, Last sequence up
01-FEB-1996 (Rel. 33, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIDFILIKNNLFLGKIFWVF 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-92114051; Pubmed-1731062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marchantia polymorpha (Liverwort) Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=93247547; Pubmed=8483448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -IFWIF 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Η.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.8%;
llarity 45.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome.";
223:1-7(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marchantiopsida; Marchanti
Marchantiaceae; Marchantia
NCBI_TaxID=3197;
                                                                                                                                                                                                                                                                                      EMBL; U67521; AAB98753.1;
TIGR; MJ0762; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oda K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIDFI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OR NAD4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NU4M_MARPO
P26848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nozato N.,
                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF03
TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Mol.
THE PRESENTATION OF THE PROPERTY AND DOCUMENT AND DESCRIPTION OF THE PROPERTY AND DESCRIPTION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                its
                                in no way commercial
                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gigartinaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          + ubiquinol.
                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ή
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the rhodophyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grienenberger
                                                                                                                                                                                                                                          Length 495;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chondrus crispus (Gigartinales). Gene content and genome organization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                             ; Mitochondrion.
0F75894D6CAAAED4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gigartinales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
(EC 1.6.5.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ubiquinone = NAD(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00361; oxidored_q1; 1.
Pfam; PF00662; oxidored_q1_N; 1.
PRINTS; PR01434; NADHDHGNASE5.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEROITENCE 666 AA; 75628 MW; 37E86F2C24B9D360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leblanc C., Boyen C., Richard O., Bonnard G., G
Kloareg B.;
"Complete sequence of the mitochondrial DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                          666 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40.5; D. Pred. No. 48; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                          ore 41; DB ed. No. 31; Mismatches
                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion.
Eukaryota; Rhodophyta; Florideophyceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
NADH-ubiquinone oxidoreductase chain 5
                                                                                                     EMBL; M68929; AAC09398.1; -. PIR; S25942; S25942. InterPro; IPR003918; NADHub_oxred4. InterPro; IPR001750; Oxidored_q1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 247547; CAA87625.1; -.
InterPro; IPR003916; NADHub_oxred5.
InterPro; IPR001750; Oxidored_q1.
InterPro; IPR001516; Oxidored_q1.
                                                                                                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Apices;
MEDLINE=95341681; PubMed=7616569;
                                                                                                                                                                                                Ubiquinone;
56311 MW; 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dol. Biol. 250:484-495(1995)
CATALYTIC ACTIVITY: NADH +
                                                                                                                                                                                                                                                                        5
                                                                                                                                                               Pfam; PF00361; oxidored_q1; 1
PRINTS; PR01437; NUOXDRDTASE4
Oxidoreductase; NAD; Ubiquinol
SEQUENCE 495 AA; 56311 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                crispus (Carragheen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.3%;
ilarity 53.3%;
Conservative
                                                                                                                                                                                                                                           41.8%; 41.7%;
                                                                                                                                                                                                                                                                                                                     | :| :||::|:
CSLDLLIFYVFF 146
                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                    CGIDFIIFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                         Similarity 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity es 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=2769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ND5 OR NAD5.
Chondrus cri
                                                                                                                                                                                                                                                                                                                                                                                                           NU5M_CHOCR
P48920;
                                                                                                                                                                                                                                                                                                                                  135
                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chondrus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best
                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                           /5M_(
 qq
                                                                                                                                                                                                                                                                                                       δ
```

```
TRANSMEM
                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                    RAT
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
DCE1_RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                             collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                        for commercial
                                                                                                                                                                                                                                                                                                                                                                 sib.ch/announce,
                                                                                                                                                                                                                                                                                                                          MBL outstation
                                                                                                                                                                                                                                                                                                                                   restrictions on
                                                                                                                                                                                                                                                                                                                                               no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                    ۲٠.
ات
                                                                                                                                                                                                                                                                                                                                               in
                                                                                                                                                                                                                                                                               TEIN IN
                                                                                                                                               Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                of the
                                                                                                                                                                                                                                     III, Blattner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . A.,
                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=94316500; PubMed=8041620;
Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blat "Analysis of the Escherichia coli genome. V. DNA sequence region from 76.0 to 81.5 minutes.";
Nucleic Acids Res. 22:2576-2586(1994).
-! SIMILARITY: STRONG, TO E.CHRYSANTHEMI HYPOTHETICAL PROTROGK 5'REGION (AC P45417).
                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by ancentities requires a license agreement (See http://www.isb-sorted an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gocayne J.D., White O., Adams M.D., Clayton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
on update)
                                                                       July CT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yhjb.
YHJD OR B3522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oi-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence ug
16-OCT-2001 (Rel. 40, Last annotation
Hypothetical protein MG147.
MG147.
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U00039; AAB18498.1; -.
EMBL; AE000428; AAC76547.1; -.
ECOGene; EG12248; yhjD.
InterPro; IPR005274; Cons_hypoth766.
InterPro; IPR004664; RNase_BN.
Pfam; PF03631; Ribonuclease_BN; 1.
TIGRFAMS; TIGR00766; TIGR00766; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37911 MW;
                    189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.8%;
          | : || |:|||:|
FGLSLGI-FLIFWVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
FOANCGIDFIIFWIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piam, TigRuu, C., TigRuu, C., Hypothetical protein; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 IIFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : |||||
LFFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P47393;
01-FEB-1996
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser C.M.,
                                                                                                                                                                     Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y147_MYCGE
                   176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                     RESULT
                                                             YHJD_]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC
DT
DT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DT
DE
GN
                                                                                                                                                                                                                                                                  #0000000000000
                                                                                                                                                                                                                                                                                                                                                                                                           П
                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                    q
δ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                     J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus
   Kelley J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning, characterization, and autoimmune recognition of rat islet
glutamic acid decarboxylase in insulin-dependent diabetes mellitus.
                        b
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J. Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J. Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; "The minimal gene complement of Mycoplasma genitalium."; Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GAD-67)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  deduced from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E., Moldrup A., Dyrberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                      Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A14AF07D574E8046 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .1.1.15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glutamic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sedneuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Glutamate decarboxylase, 67 kDa isoform (EC 4 (67 kDa glutamic acid decarboxylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             593 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D.I.;
for rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brain Res. 8:193-198(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Co
| POTENTIAL.
5
                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Julien J.F., Samama P., Mallet J.; "Rat brain glutamic acid decarboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Michelsen B.K., Petersen J.S., Boel Madsen O.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91014554; PubMed=2170798; Wyborski R.J., Bond R.W., Gottlieb "Characterization of a cDNA coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90132703; PubMed=2299361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurochem. 54:703-705(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43188 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.8%;
                                                                                                                                                                                                                                                                                                             EMBL; U39695; AAC71365.1;
TIGR; MG147; -.
Hypothetical protein; Tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                       41
86
181
223
223
254
309
358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 DFILFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||:: |||:
239 DFLVLWIFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Α.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
hes 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                       66
1161
203
234
289
338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brain Res. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           decarboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DCE1_RAT
P18088;
01-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RN
RX
RA
RA
RT
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                      GAD, HDC AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                         EMBL; M34445; AAC42037.1; ...

EMBL; M36475; CAA40801.1; ...

EMBL; X57573; CAA40801.1; ...

EMBL; X57573; CAA40801.1; ...

EMBL; X57573; CAA40801.1; ...

EMBL; M56177; AAA41184.1; ...

EMBL; M56177; AAA41184.1; ...

EMBL; M43756; A43756.

R InterPro; IPR002129; Pyridoxal_dec. 1:

R PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.

R POOFICT and total tigene family.

BINDING 404 PYRIDOXAL PHOSPHATE (POTENTIAL).

CONFLICT 284 284 EH -> AD (IN REF. 2).

CONFLICT 287 288 EH -> AD (IN REF. 2).

CONFLICT 344 345 AG -> EA (IN REF. 2).

T CONFLICT 343 347 T -> I (IN REF. 2).

T CONFLICT 344 345 AG -> LE (IN REF. 2).

T CONFLICT 380 380 L -> R (IN REF. 2).

SEQUENCE 593 AA; 66640 MW; EF83239C30301F69 CRC64;
                                             CO(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 593;
c. Natl. Acad. Sci. U.S.A. 88:8754-8758(1991).
FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CATALYTIC ACTIVITY: L-glutamate = 4-aminobutanoate +
COFACTOR: PYRIDOXAL PHOSPHATE.
SUBUNIT: HOMODIMER.
SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, TYRDC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 1;
Pred. No. 52;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 CGRHVDIFKFWLMW 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CG--IDFILFWIFW 16
   Proc
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

Search completed: July 9, 2003, 15:08:58 Job time : 11.9823 secs

```
5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2003
```

using sw model - protein search, OM protein

Seconds 9, 2003, 15:05:28 ; Search time 7.22124 S (without alignments) 456.536 Million cell July Run on:

updates/sec

US-09-854-133-587 98 1 FQANCGIDFIIFWIFW 16 Title: Perfect score:

Scoring table:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

671580 seqs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Databasė

SPTREMBL_21:*

sp_archea:*
sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_phage:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q9p9f4 methanosarc	Q8tqn5 methanosarc	Q9tdu3 echinococcu	Q9ev68 rhizobium m	Q92yn6 rhizobium m	Q958u2 echinococcu	Q8t411 brugia mala	Q8vev1 mus musculu	Q953m3 echinococcu	Q9rph1 escherichia	Q9rm48 escherichia	Q8vqr2 escherichia	Q8vnr6 escherichia	Q968z8 plasmodium	Q91zb6 mus musculu	Q96am1 homo sapien
ID	Q9P9F4	Q8TQN5	O9TDU3	O9EV68	092YN6	095802	Q8T4L1	Q8VEV1	Q953M3	Q9RPH1	Q9RM48	Q8VQR2	Q8VNR6	0968z8	Q912B6	Q96AM1
DB	-	1.7	ω	7	16	ω	ស	11	æ	7	7	7	~	Ŋ	11	4
Length	495	495	275	491	491	535	192	310	530	3223	3223	3223	3223	269	319	343
% Query Match	. 0	·.	48.0	Ξ. œ	ω	ω	9	٠,	9	9	9	9	•	5	45.9	5.
Score	49	49	47	47	47	47	46	, 46	46	46	46	46	46	45	45	45
Result No.		2	m	4	J.	9	7	ω	σ	10	11	12	13		15	

Score 49; DB 1; Length 495; Pred. No. 7.9;

50.0%; 60.0%;

Query Match Best Local Similarity

Q8vcj6 mus muscu 9na34 caenorhabd 02708 podospora 031816 bacillus 097101 clostridi 9u8r4 drosophila 95xs9 caenorhabd 9v3s5 drosophila 9u4g2 homo sapie 9uhq2 homo sapie 9uhq3 homo sapie 9uhq3 homo sapie 9uhq3 homo sapie 9uhq3 homo sapie 09ry3 homo sapie 09ry3 homo sapie 09ry1 helicobac 09pma3 campyloba 09pma3 campyloba 09fj20 arabidops 09fj20 arabidops 09sb30 arabidops	204 SC 875 Ca 097 th 7661 x fmn5 a 181 ve
45 45.9 343 11 Q8VCJ6 45 45.9 856 5 Q9NA34 44 44.9 179 16 O31816 44 44.9 391 16 Q97L01 44 44.9 531 5 Q9U8R4 44 44.9 1440 5 Q9U8R4 43 43.9 167 4 Q9UHQ2 43 43.9 221 4 Q9UHQ3 43 43.9 221 4 Q9UHQ3 43 43.9 221 4 Q9UHQ3 43 43.9 221 6 Q95KW8 43 43.9 503 17 Q9PMA3 43 43.9 503 17 Q9PMA3 43 43.9 516 17 Q9FJZ0 42 42.9 194 16 Q8YPS8 42 42.9 256 10 Q9SB30	2 42.9 351 5 076 2 42.9 386 3 093 2 42.9 483 8 Q36 2 42.9 622 13 05 2 42.9 671 10 Q9 1 41.8 103 8 Q9G
111122222222222 12832210988888888888888888888888888888888888	0 4 4 4 4 0 1 2 2 4 4 5 5 4 5 4 5

ALIGNMENTS

```
PRELIMINARY;
                                                                                                                                                                                                                                                           275
275 AA;
                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001
01-MAR-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=RM41;
                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127
                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF
PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9EV68;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9EV68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          092YN6
                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAD;
                                                                                                                                                                                                                                                           NON
                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                                                                                                                                                                                                                                                                                                              Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
Q92YN6
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                          Q9EV68
       ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΩI
      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                              Ye W.,
Guss A.M.,
                                                                                                                                                                                                                                                                        STRAIN—CLA / ATCC 35395 / DSM 2834;

X REDLINE—21929760; PubMed=11932238;

X Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P., Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Atnoor D., Brown A., Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R., Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A., A Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I., Fritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., Metcalf W.W. Birren B.;

"The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity.";

Genome Res. 12:532-542(2002).

R EMBL; AE010819; AAM04919.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESPIRATORY SUBUNITS 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                    metabolic
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF THE WATER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ogrbu3;
Ogrbu3;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
     Indels
                                                                                                                                                                                                   Methanosarcina acetivorans.
Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cestoda; Eucestoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278918B16BA7BAE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=21036605; PubMed=11163447;
Nakao M., Sako Y., Yokoyama N., Fukunaga M., Ito A.;
Nakao M., Sako Y., Yokoyama N., Fukunaga M., Ito A.;
"Mitochondrial genetic code in cestodes.";
Mol. Biochem. Parasitol. 111:415-424(2000).
-!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO
                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
F(420)H(2) dehydrogenase, subunit FpoM.
FPOM OR MA1505.
     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49; DB 17;
Pred. No. 7.9;
1; Mismatches (
                                                                                                                  495 AA
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Platyhelminthes; Ce;
Cyclophyllidea; Taeniidae; Echinococcus
NCBI_TaxID=6210;
   4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54138 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.08;
  Conservative
                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :||::|:||
128 LDFVVFYIFW 137
                         IDFILEWIEW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 IDFIIFWIFW 16
                                     :||::|:||
128 LDFVVFYIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Local 6; Conserva
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome. SEQUENCE 495 AA;
                                                                                                                                                                                                                                           NCBI_TaxID=2214;
 9
                                                                                                               OBTONS
OBTONS;
Matches
                                                                                       RESULT
                                                                                                   Q8TQN5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9TDU3
                                                  g
                                                                                                                                                   RA
RA
                          ŏ
                                                                                                                                                                                                                                                                                                                               RA
RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <del>Q</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DT
DT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 000
000
000
000
000
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                            -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME
C + 2 H(2)O.
-!- COFACTOR: HEMES A, A3, AND COPPER B (BY SIMILARITY).
-!- COFACTOR: HEMES A, A3, AND COPPER B (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
INNER MEMBRANE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
REMBL; AB033407; BAA85324.1; -.
RINTERPOOL BAA85324.1; -.
RINTERPOOL BAA85324.1; -.
REMBL; AB033407; BAA85324.1; -.
REMBL; AB033407; COXI: UNKNOWN_I.
REMBL; PROUNT; COXI: UNKNOWN_I.
RESPIRATORY Chain; Transmembrane.
                                                                                                                      4 FERRICYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME AND COPPER B (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putnoky P., Jady B., Chellapilla K.P., Barta F., Kiss E.; "Sinorhizobium meliloti carries two sets of nuo genes."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-! CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
-! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY) EMBL; AJ245399; CAC14150.1; -. InterPro; IPR003918; NADHUD_oxred4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20B1917902CB529D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Ubiquinone.
2714 MW; A2C62574220C4EEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative NADH-ubiquinone oxidoreductase subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47; DB 8
Pred. No. 9.5;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30298 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00361; oxidored_q1; 1
S; PR01437; NUOXDRDTASE4
Oxidoreductase; Transmem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52714 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGIDFIIFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FQANCGIDFIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ::||:||:|
FSSSCGVDFLMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | :| :|::||
CALDLFLFYVFW
```

491 AA.

PRT;

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRICYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESPIRATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNITS
IS THE
IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF SUBUNIT
ED BY HEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wells D.H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COFACTOR: HEMES A, A3, AND COPPER B (BY SIMILARITY).
PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
INNER MEMBRANE (BY SIMILARITY).
SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAM
i, AF297617; AAK51685.1; -.
                                                                                                                                                                                                                                           group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21396509; PubMed=11481432;
Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.]
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Werth K.-C., Davis R.W., Federspiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti pSymA megaplasmid.";
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
EMBL; AE007270; AAK65494.1; -.
InterPro; IPR001750; Oxidored_q1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Le T.H., Blair D., Dai N.T.H., Pearson M., McManus D.P.;
"Echinococcus mitochondrial genome.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER.
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  491
                                                                                   update)
( I) oxidoreduc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 FE
                                                                                                                                                                                                            Plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cestoda; Eucestoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        + 0(2) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       el. 19, Last sequence update)
el. 20, Last annotation update)
polypeptide I (EC 1.9.3.1).
Q92YN6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
NuoM2 NADH-ubiquinone/plastoquinone (Complex I) o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOCHROME C ARE TRANSFERRED VIA THE COPPIAND HEME A OF SUBUNIT 1 TO THE BIMETALLIC AND COPPER B (BY SIMILARITY).

CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ore 47; DB : ed. No. 16; Mismatches
                                                                                                                  NUOM2 1.6.5.3).
NUOM2 OR RA0836 OR SMA1536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Platyhelminthes; Cest
Cyclophyllidea; Taeniidae; Echinococcus.
NCBI_TaxID=6210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00361; oxidored_q1.
Oxidoreductase; Plasmid; Complete SEQUENCE 491 AA; 5202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₹;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 19, (TrEMBLrel. 19, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.0%;
ilarity 41.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :| :|::||
CALDLFLFYVFW 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 CGIDFILFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                granulosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C + 2 H(2)0.
COFACTOR: HE
                                                                                                                                                                                                                                                                 Rhizobiaceae; S
NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Echinococcus Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q958U2,
Q958U2,
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FR
STRAIN=1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        !
-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
0958U2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DE DE CO DE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RA
RT
RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
```

EMBL;

```
Gaps
                                                                                                                                                                                                                                                                                                                       Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vertebrata; Euteleostomi;
                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murinae;
InterPro; IPR000883; COX1.
Pfam; PF00115; COX1; 1.
PRINTS; PR01165; CYCOXIDASEI.
PROSITE; PS00077; COX1; UNKNOWN_1.
Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane.
SEQUENCE 535 AA; 60100 MW; 49944A4882F4FCED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams M.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY073797; AAL61460.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Wu Y., Bianco A.E.;

Wu Y., Bianco A.E.;

"Thioredoxin of human filarial parasite Brugia malayı.";

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ cRC64;

EMBL; AY080907; AAL91107.1; -.

EMBL; AY080907; AAL91107.1; -.

192 AA; 22071 MW; 617B22FA86BCEA01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ۵
                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
on update)
                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                             .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ore 46; DB 5 ed. No. 9.8; Mismatches
                                                                                                                                                                                                                                                             sequence up
annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 AA
                                                                                           DB
18;
                                                                                                                                                                                                                                                                                                                       Nematoda; Chromadorea;
                                                                                                                    Mismatches
                                                                                                                                                                                                                           192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       superfamily
                                                                                           Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                            Last
Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Cre
01-MAR-2002 (TrEMBLrel. 20, Las
01-JUN-2002 (TrEMBLrel. 21, Las
01factory receptor MOR261-11.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Rodentia; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang X., Firestein S.J.; "The olfactory receptor gene Nat. Neurosci. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.9%;
                                                                                             48.0%;
50.0%;
                                                                                                                                                                                                                                                  21,
21,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANCGIDFIIFWIFW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                    Conservative
                                                                                                                                          12
                                                                                                                                                                                                                                                (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ||:: ||:| |:
AYCGLNEIIYWYFY
                                                                                                                                                                                                                            PRELIMINARY
                                                                                                                                                                                                                                                                                                          Brugia malayi.
Eukaryota; Metazoa; Ner
Onchocercidae; Brugia.
NCBI_TaxID=6279;
                                                                                                                                           FOANCGIDFIIF
                                                                                                                                                       | ::||:||
| 38 FSSSCGVDFLMF
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
7; Conserve
                                                                                                        Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8VEV1;
01-MAR-2002
01-MAR-2002
01-JUN-2002
                                                                                                                                                                                                                                      Q8T4L1;
01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                    Thioredoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ო
                                                                                                                                           Н
                                                                                             Query Match
                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8VEV1
                                                                                                                                                                                                                            Q8T4L1
                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                TRX
                                                                                                                                                                                                    RESULT
Q8T4L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8VEV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pp
   DR
DR
DR
XW
XW
SQ
                                                                                                                                                                  Dp
                                                                                                                                             Qλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
```

```
NCBI_TaxID=562
                                                                                                                                                                                                                                                                                                                                                                                                                   Lymphostatin.
LIFA.
Escherichia co
                                                                                                                                                                                                                                                                                                                                                             Q9RM48;
Q9RM48;
01-MAY-2000
01-MAY-2000
      factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8VQR2
Q8VQR2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
Q8VQR2
                                                                                                                                                                                                                                                                                                                                            RESULT
     AC
DT
DT
DT
DE
                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        엄
                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                        2
A3
                                                                                                                                                                                                                                                                                                                                                              RESPIRATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                      4 FERRICYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASE FAMILY
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  BY HEME
                                                                                                                                                                                                                                                                                                                                                                          SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                            C + 2 H(2)O.

COFACTOR: HEMES A, A3, AND COPPER B (BY SIMILARITY).

PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).

SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAM.

L, AF346403; AAK82350.1; -.

erPro; IPR000883; COX1.

m; PF00115; COX1; 1.
                                                                                                                                                                                                                                                                                                                                                                                   IS THE
                                                                                                                                                                                                                                                                                                Le T.H., Dai T.H.N., Blair D., McManus D.P.;

"Complete mitochondrial genome of Echinococcus granulosus (G4 genotype).";

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESE CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBC.

3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS TATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUB AND COPPER B (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYT C + 2 H(2)O.

-!- COFACTOR: HENDER P.
                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                             310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00077; COX1; UNKNOWN_1.
COPPEr; Heme; Inner membrane; Mitochondrion; Oxidoreductase
Respiratory chain; Transmembrane.
                                                                                                                                                                                          ol-DEC-2001 (TrEMBLrel. 19, Last Sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Cytochrome c oxidase polypeptide I (EC 1.9.3.1) (Fragment)
COX1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 530;
                                                                   Indels
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
Cyclophyllidea; Taeniidae; Echinococcus.
NCBI_TaxID=6210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                             Length
                        452A1D723081781D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2E5FCA534DFD1771 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation updat
                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <del>ω</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3223 AA.
                                           ore 46; DB ed. No. 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ed. No. 25;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
  G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46;
Pred. No.
                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                            Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred
                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                      34917 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01165; CYCOXIDASEI.
PROSITE; PS00077; COX1; UNKNC
COPPER; Heme; Inner membrane;
                                                                                                                                                                                    (TrEMBLrel. 19, (TrEMBLrel. 19, 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 13, C (TrEMBLrel. 13, I (TrEMBLrel. 20, I
                                          46.9%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.9%;
llarity 50.0%;
Conservative
                                                                                                            30
                                                                                      2 QANCGIDFIIFWIF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144
                                                                 Conservative
                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
                                                                                                  | : ||: :||||
QLSAGIEMFLFWIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                         Echinococcus granulosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | : ||:||:|
FSSGCGVDFLMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOANCGIDFIIF
                      310 AA;
                                                     Local Similarity
les 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Matcn
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 530 AA;
PS50262;
                                                                                                                                                                                                                                                   Mitochondrion
                                                                                                                                                                       Q953M3;
01-DEC-2001
01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9RPH1;
01-MAY-2000
01-MAY-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133
            Receptor
 PROSITE;
                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                Q953M3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9RPH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
Q9RPH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <del>1</del> <del>1</del> <del>1</del>
                                                       Best
                                                                                                                                          RESULT
0953M3
                                                                                                          q
                                                                                                                                                                                                                   OE
GN
                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           П
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC
DT
DT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                   col1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                            locus that is required for in enterohaemorraghic Escherichia
                                                          gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strains that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McNamara B.P., Lai L.C.,
                                                                                                                                                                             MEDLINE-20117988; PubMed=10652089;
Nicholls L., Grant T.H., Robins-Browne R.M.;
"Identification of a novel genetic locus that is required for adhesion of a clinical isolate of enterohaemorraghic Escherito epithelial cells.";
Mol. Microbiol. 35:275-288(2000).
EMBL; AF159462; AAD49229.2; -.
InterPro; IPR001917; NHtransf_2.
InterPro; IPR00169; SHprot_acsite.
PROSITE; PS00599; AA_TRANSFER_CLASS_2; UNKNOWN_1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
SEQUENCE 3223 AA; 365949 MW; CAFD59F69242D07A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=E2348/69;
MEDLINE=20187489; PubMed=10722613;
Klapproth J.M.A., Scaletsky I.C.A., McNamara B.P., Lai L.C.
Malstrom C., James S.P., Donnenberg M.S.;
"A large toxin from pathogenic Escherichia coli strains that lymphocyte activation.";
Infect. Immun. 68:2148-2155(2000).
EMBL; AJ133705; CAB55629.1;
InterPro; IPR001917; NHtransf_2.
InterPro; IPR00169; SHprot_acsite.
PROSITE; PS00599; AA_TRANSFER_CLASS_2; UNKNOWN_1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
SEQUENCE 3223 AA; 365963 MW; 03E45ECDED7938C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46; DB 2; Louis Pred. No. 1.4e+02; 4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB 2; Lk
Pred. No. 1.4e+02;
}; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3223 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16
                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 13, (TrEMBLrel. 13, (TremBlrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.98
for adherence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2163 YQANTEIEYLSNWIVW
                       EFAl.
Escherichia coli.
Bacteria; Proteobacteria;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FQANCGIDFIIFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOANCGIDFIIFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match ·
Best Local Similarity
'`` 7; Conserv
                                                                                                                    [1]
SEQUENCE FROM N.A.
STRAIN=E45035;
MEDLINE=20117988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Watches 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=562;
```

```
RL
DR
DR
DR
SO
                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                       DT DT DT OC OC OC OC OC OC OC OC OC
                                                                                                                                                                                                                                                                                                                                                                                                                                             RP
RX
RA
RT
RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DR
DR
DR
DR
FT
                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shiga toxin-
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                aceae;
                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ő
                                                                                                                                  it
                                                                                                                                  rabb
                                                              Enterobacteri
                                                                                                                                                                                                                                  Length 3223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in
                                                                                                                                                                                                               CRC64;
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                    Tauschek M., Strugnell R.A., Robins-Browne R.M.;
"Characterization of the LEE pathogenicity islands of reenteropathogenic Escherichia coli.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF453441; AAL57562.1;
InterPro; IPR001917; NHtransf_2.
InterPro; IPR0010169; SHprot_acsite.
PROSITE; PS00599; AA_TRANSFER_CLASS_2; UNKNOWN_1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
SEQUENCE 3223 AA; 365790 MW; E97D10B98FADE658 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            II locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=413/89-1;
Benkel P., Chakraborty T.;
Benkel P., Chakraborty T.;
"Genetic organisation and sequence of the LEE II locuproducing Escherichia coli.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ database EMBL; AJ277443; CAC81883.1; -.
InterPro; IPR001917; NHtransf_2.
InterPro; IPR000169; SHprot_acsite.
PROSITE; PS00599; AA_TRANSFER_CLASS_2; UNKNOWN_1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
SEQUENCE 3223 AA; 365666 MW; 28EBB4374FAB8FC7 CRC
              sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.4e+02; ; Mismatches 5;
                                                                                                                                                                                                                                Score 46; DB 2;
Pred. No. 1.4e+02;
4; Mismatches 5
                                                 Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46;
     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
            Last
Last
                                                                                                                                                                                                                                                                                           2178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2178
                                                                                                                                                                                                                                                                         16
   20,
20,
21,
                                                                                                                                                                                                                                 46.9%;
                                                                                                                                                                                                                                                                                                                                                             20,
20,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.9%;
larity 43.8%;
Conservative
                                                                                                                                                                                                                                                                                  2163 YQANTEIEYLSNWIVW
                                                                                                                                                                                                                                                                        1 FOANCGIDFIIFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOANCGIDFIIFWIFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YQANTEIEYLSNWIVW
  (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q96828 PRELIMINARY;
Q96828;
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                          PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                           STRAIN=83/39;
Tauschek M., Strugnell
"Characterization of tl
                                                                                                                                                                                                                                                                                                                                      Q8VNR6;
Q8VNR6;
Q1-MAR-2002 (TrEMBLrel
01-MAR-2002 (TrEMBLrel
01-JUN-2002 (TrEMBLrel
Efal-LifA-Tox protein.
EFAl-LIFA-TOX.
                                                                                                                                                                                                                                       Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 7; Conser
                                                                                                    N.A
                                                                                NCBI_TaxID=562;
                                                                                                   FROM
01-MAR-2002
01-MAR-2002
01-JUN-2002
Efal.
                                                                                                  EQUENCE
                                                                                                                                                                                                                                 uery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
Q96828
                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                        13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                         Best
                                                                                                                                                                                                                                                                                                                        RESULT
                    qq
                                                                                                                                                                                                                                                                                                                                          ΠD
                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HA ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                       Pos25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi
Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/6;
MEDLINE=21435808; PubMed=11551509;
Modification of GPCRs Expressed in Specific Subsets of Nociceptive Somatosensory Neurons.";
Cell 106:619-632(2001).
EMBL; AY042211; AAK91802.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
Receptor.
                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                        Σ
                                                                  P. ovale).
Haemosporida; Plasmodium.
                                                                                                                                                                                                       genes,
                                                                                                                                                                                      Torii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 319
                                                                                                                                                                                                                                                                                                                                                        Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                               SEQUENCE FROM N.A.
STRAIN=NIGERIAN I/CDC;
MEDLINE=21192570; PubMed=11295191;
Tachinbana M., Tsuboi T., Templeton T.J., Kaneko O., Tor "Presence of three distinct ookinete surface protein gen Pos28-1, and Pos28-2, in Plasmodium ovale.";
Mol. Biochem. Parasitol. 113:341-344(2001).
EMBL; AB051633; BAB43950.1; -.
InterPro; IPR000561; EGF-1ike.
SMART; SM00181; EGF; 3.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
SEQUENCE 269 AA; 29928 MW; 7A949BB42F036EEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           Indel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D1860538BA7A965C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Sciurognathi; Muridae;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Ookinete surface protein Pos28-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
(Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11;
                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                      Score 45; DB 5
Pred. No. 19;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                              Plasmodium ovale (malaria parasite
Eukaryota; Alveolata; Apicomplexa;
NCBI_TaxID=36330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003, 15:06:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U1-DEC-2001 (TrEMBLrel. 19, Cl 01-DEC-2001 (TrEMBLrel. 19, Le 01-MAR-2002 (TrEMBLrel. 20, Le G protein-coupled receptor (Frank MRGF.
                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35955 MW;
                                                                                                                                                                                                                                                                                                                                                     45.9%;
nilarity 46.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          |: || ::|:||
FKCNCTRNYIVFW 104
                                                                                                                                                                                                                                                                                                                                                                                                                        FQANCGIDFIIFW 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ď
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 GIDFILFWIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||::||:|
| S32 GIDWFLFWVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: July
Job time: 10.2212 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q91ZB6;
Q91ZB6;
01-DEC-2001
01-DEC-2001
                                                                                                                    [1]
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                          Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Job time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q912B6
```

**			